Access DB# 28495

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # :_____ Date: _____

Art Unit: _____ Phone Number 30_____ Serial Number: _____

Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

****

STAFF USE ONLY

Searcher: Shepperd

Searcher Phone #: 308-4499

Searcher Location: _____

Date Searcher Picked Up: _____

Date Completed: 5/19/00

Searcher Prep & Review Time: _____

Clerical Prep Time: _____

Online Time: _____

Type of Search

NA Sequence (#)_____

AA Sequence (#)_____

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr.Link _____

Lexis/Nexis_____

Sequence Systems _____

WWW/Internet _____

Other (specify)_____

PTO-1590 (1-2000)

28495

STIC-Biotech/ChemLib

From: Saoud, Christine
Sent: Monday, May 08, 2000 8:47 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Importance: High

09/214,982

Please search SEQ ID NO:1 and 2 in the patent and commercial databases.

Thank you,
Christine Saoud
A.U. 1646
CM1 - 10E03
305-7519

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 16, 2000, 11:41:21 ; Search time 682.87 Seconds
(without alignments)
11894.884 Million cell updates/sec

Title: US-09-214-982-2
Perfect score: 2004
Sequence: 1 ccagctttctgtarctgtaa.....aaacaccattattcaagtct 2004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*
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109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

	No.	Score	Match	Length	DB	ID	Description
c	1	429	21.4	449	38	AA813617	AA813617 ah93e02.s
	2	425.6	21.2	531	84	B15679	B15679 345M17.TV C
c	3	415.4	20.7	425	40	AA995128	AA995128 ou22a07.s
	4	374.2	18.7	419	23	H24828	H24828 yl42g02.r1
c	5	368.4	18.4	381	40	AA977475	AA977475 on60a11.s
c	6	358.2	17.9	461	21	T64149	T64149 yc09b12.s1
c	7	302.4	15.1	320	48	AI572543	AI572543 te39h02.x
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	9	285.6	14.3	393	21	T64277	T64277 yc09b12.r1
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	13	152.8	7.6	433	79	AW259096	AW259096 um85h12.y
	14	121.4	6.1	288	60	AV139144	AV139144 AV139144
	15	119.6	6.0	248	34	AA458208	AA458208 vg45g02.r
	16	119	5.9	509	33	AA425486	AA425486 zw46b06.r
	17	114.6	5.7	495	69	AW142056	AW142056 EST292271
	18	114.2	5.7	463	69	AW140360	AW140360 EST290322
c	19	109.2	5.4	472	43	AI170324	AI170324 EST216250
	20	106.6	5.3	253	72	AV290295	AV290295 AV290295
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	22	96.2	4.8	351	29	AA168177	AA168177 ms43f10.r
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	34	75.2	3.8	321	60	AV168534	AV168534 AV168534
	35	71.2	3.6	400	31	AA298283	AA298283 EST113896
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	45	52.4	2.6	258	29	AA149461	AA149461 zl27h03.r

ALIGNMENTS

RESULT 1
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LOCUS AA813617 449 bp mRNA EST 31-DEC-1998
DEFINITION ah93e02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1326650 3', mRNA sequence.
ACCESSION AA813617
VERSION AA813617.1 GI:2882302
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 449)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 964 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 428.

FEATURES Location/Qualifiers
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/clone="IMAGE:1326650"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 149 a 89 c 85 g 126 t
ORIGIN

Query Match 21.4%; Score 429; DB 38; Length 449;
Best Local Similarity 98.7%; Pred. No. 4.8e-104;
Matches 443; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy   1615 agctaaggagtccctggttcattgatggatgtcttctagctgcagatgcctctgcgcacc 1674
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Qy   1675 aaggaatggagaggaggggacccatgtaatccttttgtttagttttgttttgttttttg 1734
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Qy   1735 gtgaatgagaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattactcaga 1794
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Qy   1795 gcagatgaggaaaactgtagtctctgagtcctttgctaatcgcaactcttgtgaattatt 1854
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Qy   1855 ctgattctttttttatgcagaatttgattcgtatgatcagtactgactttctgattactgt 1914
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Qy   1915 ccagcttatagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtatt 1974
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Db     89 CCAGCTTATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTATT 30

Qy   1975 taaagaaaataaacaccattattcaagtc 2003
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Db     29 TAAAGAAAATAAACACCATTATTCAAGCC 1
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RESULT 2
B15679
LOCUS B15679 531 bp DNA GSS 04-JUN-1998
DEFINITION 345M17.TV CIT978SKA1 Homo sapiens genomic clone A-345M17, genomic survey sequence.
ACCESSION B15679
VERSION B15679.1 GI:2123428
KEYWORDS GSS.
SOURCE human.

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Adams,M.D., Kelley,J.M., Rounsley,S.R. and Venter,J.C.
  TITLE     Use of a BAC End Sequence Database for Sequence-Ready Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /sex="Female"
                     /cell_type="Fibroblast"
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BASE COUNT      145 a     95 c    110 g    179 t      2 others
ORIGIN
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  Query Match             21.2%;  Score 425.6;  DB 84;  Length 531;
  Best Local Similarity   96.1%;  Pred. No. 4e-103;
  Matches  465;  Conservative    2;  Mismatches   13;  Indels    4;  Gaps    3;

Qy       1 ccagctttctgtarctgtaagcattggtggccacaccacctccttacaaagcaactag-a 59
           ||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||| |
Db      51 CCAGCTTTCTGTACCTGTAACCATTGGTGGCCACACCACCTCCTTACAAAGCAACTAGAA 110

Qy      60 acctgcggcatacattggagagatttttttaatttttctggacaygaagtaaatttagagt 119
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Db     111 ACCTGCGGCATACATTGGAGAGATTTTTTTAATTTTCTGGACATGAAGTAAA-TTAGAGT 169

Qy     120 gctttcyaatttcaggtagaagacatgtccaccttctgattatttttggagaacattttg 179
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Db     170 GCTTTCTAATTTCAGGTAGAAGACATGTCCACCTTCTGATTATGTGTGGAGAACATGTTG 229

Qy     180 attttttttcatctctctctccccaccccctaagattgtgcaaaaaaagcgtaccttgccta 239
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Qy     360 gatgtcaactgcttagtaatcagtggatattgaaatattcaaaatgtacagagagtgggt 419
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Qy     480 tgga 483
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Db     528 TGGA 531
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RESULT   3
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LOCUS       AA995128      425 bp    mRNA            EST       27-AUG-1998
DEFINITION  ou22a07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1626996 3', mRNA sequence.
ACCESSION   AA995128
VERSION     AA995128.1  GI:3181617
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 425)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 5, 1995 this sequence version replaced gi:797630.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1376   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 413.
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                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT      144 a     87 c     77 g    117 t
ORIGIN
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Qy    1648 ttctagctgcagatgcctctgcgcaccaaggaatggagaggaggggacccatgtaatcct 1707
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Qy    1708 tttgtttagttttgtttttgttttttggtgaatgagaaaggtgtgctggtcatggaatgg 1767
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Qy    1768 caggtgtcatatgactgattactcagagcagatgaggaaaactgtagtctctgagtcctt 1827
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Qy    1828 tgctaatcgcaactcttgtgaattattctgattctttttttatgcagaatttgattcgtat 1887
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Db     185 TGCTAATCGCAACTCTTGTGAATTATTCTGATTCTTTTTTATGCAGAATTTGATTCGTAT 126
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Qy   1888 gatcagtactgacttttctgattactgtccagcttatagtcttccagtttaatgaactacc 1947
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Db    125 GATCAGTACTGACTTTCTGATTACTGTCCAGCTTATAGTCTTCCAGTTTAATGAACTACC 66

Qy   1948 atctgatgtttcatatttaagtgtatttaaagaaaataaacaccattattcaagtct 2004
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     65 ATCTGATGTTTCATATTTAAGTGTATTTAAAGAAAATAAACACCATTATTCAAGCCT 9


RESULT   4
H24828
LOCUS       H24828         419 bp    mRNA            EST       07-JUL-1995
DEFINITION  yl42g02.r1 Soares breast 3NbHBst Homo sapiens cDNA clone
            IMAGE:160946 5', mRNA sequence.
ACCESSION   H24828
VERSION     H24828.1  GI:893727
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 948
            High quality sequence stops: 384
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 948   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 384.
FEATURES             Location/Qualifiers
     source          1. .419
                     /organism="Homo sapiens"
                     /db_xref="GDB:575039"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:160946"
                     /clone_lib="Soares breast 3NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     20. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      115 a    111 c     89 g    100 t      4 others
ORIGIN


  Query Match             18.7%;  Score 374.2;  DB 23;  Length 419;
  Best Local Similarity   96.6%;  Pred. No. 2.1e-89;
  Matches  401;  Conservative    0;  Mismatches   12;  Indels    2;  Gaps    2;

Qy   1151 ctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaagatcgttgcg 1210
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTCATCTCCAGGAACCAGCTCTCTGTGGGCCACACATGATGTTTGACGAAGATCGTTGCG 60

Qy   1211 agtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaaaactgcagtt 1270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAATCCAGCACCCCAAAAACTGCAGTT 120

Qy   1271 gctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagctatttcacccag 1330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCTGCCAGAAGCACAAGCTATTTCACCCAG 180

Qy   1331 acacctgcagctgtgaggacagatgccccttttcataccagaccatgtgcaagtggcaaaa 1390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    181 ACACCTGCAGCTGTGAGGACAGATGCCCCTTTCATACCAGACCATGTGCAAGTNGCAAAA 240

Qy   1391 cagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccagggggccccaca 1450
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    241 CAGCATGTGCAAAGCATTGCCGCTTTCCAAAGGNGAAAAGGGCTGCCCAGGGGCCCCACA 300

Qy   1451 gccgaaagaatccttgattcagcgttccaagttccccatccctg-tcatttttaacagca 1509
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    301 GCCGAAAGAATCCTTGATTCAGCGTTCCAAGTTCCCCATCCCTGTTCATTTTTAACAGCA 360

Qy   1510 tgctgctttgccaag-ttgctgtcactgtttttttcccaggtgttaaaaaaaaaa 1563
          |||||||||||||| |||||||||||||||||| | | || |||| ||
Db    361 TGCTGCTTTGCCAAGTTTGCTGTCACTGTTTTTTTTNCCAGGGTGTTTAAAANAA 415


RESULT   5
AA977475/c
LOCUS       AA977475       381 bp    mRNA            EST       26-AUG-1998
DEFINITION  on60a11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1561052 3', mRNA sequence.
ACCESSION   AA977475
VERSION     AA977475.1  GI:3154921
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 381)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1877819.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 981   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 295.
FEATURES             Location/Qualifiers
     source          1. .381
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1561052"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
```

```
BASE COUNT      137 a     84 c     63 g     97 t
ORIGIN


  Query Match             18.4%;  Score 368.4;  DB 40;  Length 381;
  Best Local Similarity   99.5%;  Pred. No. 7.3e-88;
  Matches  380;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy   1622 gagtccctggttcattgatggatgtcttctagctgcagatgcctctgcgcaccaaggaat 1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GAGTCCCTGGTTCATTGATGGATGTCTTCTAGCTGCAGATGCCTCTGCGCACCAAGGAAT 322

Qy   1682 ggagaggaggggacccatgtaatccttttgtttagttttgttttttgtttttttggtgaatg 1741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 GGAGAGGAGGGGACCCATGTAATCCTTTTGTTTAGTTTTGTTTTTGTTTTTTGGTGAATG 262

Qy   1742 agaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattactcagagcagatg 1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 AGAAAGGTGTGCTGGTCATGGAATGGCAGGTGTCATATGACTGATTACTCAGAGCAGATG 202

Qy   1802 aggaaaactgtagtctctgagtcctttgctaatcgcaactcttgtgaattattctgattc 1861
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    201 AGGAAAACTGTAGTCTCTGAGTCCTTTG-TAATCGCAACTCTTGTGAATTATTCTGATTC 143

Qy   1862 ttttttatgcagaatttgattcgtatgatcagtactgactttctgattactgtccagctt 1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 TTTTTTATGCAGAATTTGATTCGTATGATCAGTACTGACTTTCTGATTACTGTCCAGCTT 83

Qy   1922 atagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtatttaaagaa 1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 ATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTATTTAAAGAA 23

Qy   1982 aataaacaccattattcaagtc 2003
          ||||||||||||||||||| |
Db     22 AATAAACACCATTATTCAAGCC 1


RESULT   6
T64149/c
LOCUS       T64149          461 bp    mRNA            EST       17-FEB-1995
DEFINITION  yc09b12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
            IMAGE:80159 3', mRNA sequence.
ACCESSION   T64149
VERSION     T64149.1  GI:668014
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 330
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -21m13
            High quality sequence stop: 330.
FEATURES             Location/Qualifiers
     source          1. .461
                     /organism="Homo sapiens"
                     /db_xref="GDB:483776"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:80159"
                     /clone_lib="Stratagene lung (#937210)"
                     /sex="male"
                     /dev_stage="72 years"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. normal lung.  Average insert size: 1.0 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT      140 a     91 c    101 g    126 t      3 others
ORIGIN


  Query Match             17.9%;  Score 358.2;  DB 21;  Length 461;
  Best Local Similarity   92.3%;  Pred. No. 4.1e-85;
  Matches  419;  Conservative    0;  Mismatches   31;  Indels    4;  Gaps    4;

Qy   1553 taaaaaaaaaatccattttacacagcaccacagtgaatccagaccaaccttccattcaca 1612
          |||||||||||  ||  ||  |||||||  ||||||||||||||  ||  |  |  |||  |||||
Db    454 TAAAAAAAAAACCCCATTNACACAGCCCCACAGTGAATCCAAGCCCAACCTCCCATCACA 395

Qy   1613 ccagctaaggagtccctggttcattgatggatg-tcttctagctgcagatgcctctgcgc 1671
          ||     | |   |||  | |||||||  |||||  ||  ||||||||||||||||||||
Db    394 CCCAGCCAAGGAGCCCCCGGTCATTGANGGATGCCCCTCCTAGCTGCAGATGCCTCTGCGC 335

Qy   1672 a-ccaaggaatggagaggagggga-cccatgtaatccttttgtttagttttgtttttgtt 1729
          | ||||||||||||||||||||  |||||||||  ||||||||||||||||||||||||||
Db    334 ACCCAAGGAATGGAGAGGAGGGGACCCCATGTAANCCTTTTGTTTAGTTTTGTTTTTGTT 275

Qy   1730 ttttggtgaatgagaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattac 1789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TTTTGGTGAATGAGAAAGGTGTGCTGGTCATGGAATGGCAGGTGTCATATGACTGATTAC 215

Qy   1790 tcagagcagatgaggaaaactgtagtctctgagtcctttgctaatcgcaactcttgtgaa 1849
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    214 TCAGAGCAGATGAGGAAAACTGTAGTCTCTGAGTCCTTT-CTAATCGCAACTCTTGTGAA 156

Qy   1850 ttattctgattctttttttatgcagaatttgattcgtatgatcagtactgactttctgatt 1909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 TTATTCTGATTCTTTTTTATGCAGAATTTGATTCGTATGATCAGTACTGACTTTCTGATT 96

Qy   1910 actgtccagcttatagtcttccagtttaatgaactaccatctgatgtttcatatttaagt 1969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     95 ACTGTCCAGCTTATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGT 36

Qy   1970 gtatttaaagaaaataaacaccattattcaagtc 2003
          ||||||||||||||||||||||||||||  || |
Db     35 GTATTTAAAGAAAATAAACACCATTATTTTAGCC 2


RESULT   7
AI572543/c
LOCUS       AI572543        320 bp    mRNA            EST       13-APR-1999
DEFINITION  te39h02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2089107
            3', mRNA sequence.
ACCESSION   AI572543
VERSION     AI572543.1  GI:4535917
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 320)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 7, 1998 this sequence version replaced gi:3121581.
```

```
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 569   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 311.
FEATURES              Location/Qualifiers
     source           1. .320
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2089107"
                      /clone_lib="Soares_NhHMPu_S1"
                      /tissue_type="Pooled human melanocyte, fetal heart, and
                      pregnant uterus"
                      /lab_host="DH10B"
                      /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; Equal amounts of plasmid DNA from three
                      normalized libraries (melanocyte 2NbHM, pregnant uterus
                      NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                      were made in vitro. Following HAP purification, this DNA
                      was used as tracer in a subtractive hybridization
                      reaction. The driver was PCR-amplified cDNAs from pools of
                      5,000 clones made from the same 3 libraries. The pools
                      consisted of I.M.A.G.E. clones 260232-265223,
                      340488-345479, and 484488-489479."
BASE COUNT      120 a     59 c     46 g     95 t
ORIGIN


  Query Match             15.1%;  Score 302.4;  DB 48;  Length 320;
  Best Local Similarity   99.7%;  Pred. No. 3.1e-70;
  Matches  303;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1700 gtaatccttttgtttagttttgtttttgtttttttggtgaatgagaaaggtgtgctggtca 1759
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    320 GTAATCCTTTTGTTTAGTTTTGTTTTTGTTTTTTTGGTGAATGAGAAAGGTGTGCTGGTCA 261

Qy   1760 tggaatggcaggtgtcatatgactgattactcagagcagatgaggaaaactgtagtctct 1819
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260 TGGAATGGCAGGTGTCATATGACTGATTACTCAGAGCAGATGAGGAAAACTGTAGTCTCT 201

Qy   1820 gagtcctttgctaatcgcaactcttgtgaattattctgattctttttttatgcagaatttg 1879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 GAGTCCTTTGCTAATCGCAACTCTTGTGAATTATTCTGATTCTTTTTTATGCAGAATTTG 141

Qy   1880 attcgtatgatcagtactgactttctgattactgtccagcttatagtcttccagtttaat 1939
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 ATTCGTATGATCAGTACTGACTTTCTGATTACTGTCCAGCTTATAGTCTTCCAGTTTAAT 81

Qy   1940 gaactaccatctgatgtttcatatttaagtgtatttaaagaaaataaacaccattattca 1999
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     80 GAACTACCATCTGATGTTTCATATTTAAGTGTATTTAAAGAAAATAAACACCATTATTCA 21

Qy   2000 agtc 2003
           || |
Db     20 AGCC 17


RESULT   8
AW261481/c
LOCUS       AW261481      463 bp    mRNA            EST       28-DEC-1999
DEFINITION  um85h12.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:2331623 3' similar to TR:P97946 P97946 VASCULAR ENDOTHELIAL
            GROWTH FACTOR D ;, mRNA sequence.
ACCESSION   AW261481
VERSION     AW261481.1  GI:6638297
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 463)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3188741.
            Other_ESTs: um85h12.y1
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1010827
            Trace considered overall poor quality
            Seq primer: custom primer used
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .463
                      /organism="Mus musculus"
                      /strain="C57BL"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:2331623"
                      /clone_lib="Sugano mouse kidney mkia"
                      /sex="female"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                      (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                      was primed with an oligo(dT) primer
                      [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                      ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                      and cloned into distinct DraIII sites of the pME18S-FL3
                      vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                      be used to isolate the cDNA insert.  Size selection was
                      performed to exclude fragments <1.5kb.  Library
                      constructed by Dr. Sumio Sugano (University of Tokyo
                      Institute of Medical Science).  Custom primers  for
                      sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                      primer CGACCTGCAGCTCGAGCACA."
BASE COUNT      113 a    102 c    127 g    121 t
ORIGIN


  Query Match             14.7%;  Score 294.6;  DB 79;  Length 463;
  Best Local Similarity   81.0%;  Pred. No. 4.1e-68;
  Matches  367;  Conservative    0;  Mismatches   84;  Indels    2;  Gaps    2;

Qy    880 tacatttccaaacagctctttgagatatcagtgcctttgacatcagtacctgaattagtg 939
          ||||| |||| |||| ||| |  |||||||||||| | |||||||||| || || |||| |
Db    463 TACATGTCCATACAGGTCTCTTCGATATCAGTGCGTCTGACATCAGTGCCCGAGTTAGGG 404

Qy    940 cctgttaaagttgccaatcatacaggttgtaagtgcttgccaacagccccccgccatcca 999
          || ||||   |||||   ||||  |||||| || ||| |||| | | ||||||||||||
Db    403 CCAGTTACCATTGCCTCCCATATGGGTTGTTAGCGCTCGCCATCGGGCCCCCGCCATCCT 344

Qy   1000 tactcaattatcagaagatccatccagatccctgaagaagatcgctgttcccattccaag 1059
          |||||||||||||||||||||| |||| ||| |||||||||   ||| | |||||||||
Db    343 TACTCAATTATCAGAAGATCCATTCAGACCCCAGAAGAAGATGAATGTCCTCATTCCAAG 284

Qy   1060 aaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgtgttttgcaggag 1119
          ||| ||||||| |||||||||| ||||||| || | |||||||||||||||||||  |
Db    283 AAATTCTGTCCGATTGACATGCTGTGGGATAACACCCAATGTAAATGTGTTTTGCAAAAC 224

Qy   1120 gaaaatccacttgctggaacagaagaccactctcatctccaggaaccagctctctgtggg 1179
          || | ||| ||  |||| |||||||||||||| | ||||||||||  ||||||||||
Db    223 GAGACTCCTCTGCCTGGGACAGAAGACCACTCTTACCTCCAGGAACCCACTCTCTGTGGA 164
```

```
Qy   1180 ccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaaaacaccatgtcccaaa 1239
          || ||||||| |||||| |||||||| || ||||| |||||||| ||||||||||   |
Db    163 CCGCACATGACGTTTGATGAAGATCGCTGTGAGTGCGTCTGTAAAGCACCATGTCCGGGA 104

Qy   1240 gatctaatccagcaccccaaaaactgcagttgctttgagtgcaaaga-aagtctggaga- 1298
          ||||| || ||||||||  |||| |||||||||||||||||||||| ||||||||||
Db    103 GATCTCATTCAGCACCCGGAAAAATGCAGTTGCTTTGAGTGCAAAGACAAGTCTGGAGAG 44

Qy   1298 cctgctgccagaagcacaagctatttcacccag 1330
          |||||||||| |    | |   |||| | | |
Db     43 CCTGCTGCCAAATTGCCCAAGAATTTTTCACCG 11


RESULT   9
T64277
LOCUS       T64277        393 bp    mRNA            EST       17-FEB-1995
DEFINITION  yc09b12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone
            IMAGE:80159 5', mRNA sequence.
ACCESSION   T64277
VERSION     T64277.1  GI:668142
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 141
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: M13RP1
            High quality sequence stop: 141.
FEATURES             Location/Qualifiers
     source          1. .393
                     /organism="Homo sapiens"
                     /db_xref="GDB:483776"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:80159"
                     /clone_lib="Stratagene lung (#937210)"
                     /sex="male"
                     /dev_stage="72 years"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. normal lung.  Average insert size: 1.0 kb;
                     Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      108 a    104 c     82 g     94 t      5 others
ORIGIN


  Query Match           14.3%;  Score 285.6;  DB 21;  Length 393;
  Best Local Similarity   92.8%;  Pred. No. 1e-65;
  Matches  321;  Conservative    0;  Mismatches   21;  Indels    4;  Gaps    2;

Qy   1222 aaaacaccatgtcccaaagatctaatccagcaccccaaaaactgcagttgctttgagtgc 1281
           |||   | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 AAACACCAATGTCCCAAAGATCTAATCCAGCACCCCAAAAACTGCAGTTGCTTTGAGTGC 62

Qy   1282 aaagaaagtctggagacctgctgccagaagcacaagctatttcacccagacacctgcagc 1341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 AAAGAAAGTCTGGAGACCTGCTGCCAGAAGCACAAGCTATTTCACCCAGACACCTGCAGC 122

Qy   1342 tgtgaggacagatgccccttcataccagaccatgtgcaagtggcaaaacagcatgtgca 1401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 TGTGAGGACAGATGCCCCTTTCATACCAGACCATGTGCAAGTGGCAAAACAGCATGTGCA 182

Qy   1402 aagcattgccgctttccaaaggagaaaaggggctgcccaggggcccccacagccgaaagaat 1461
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Db    183 AAGCATTGCCGCTTTCCAAAGGAGAAAAGGGCTGCCCAGGGGGCCCCACAGCCGAAAGGAT 242

Qy   1462 ccttgattcagcgttccaagttccccatccctgtca-tttttaacagcatgctgctttgc 1520
          |||||||||||| |||||||||| |||||||||||||| ||||||||||||||||||||
Db    243 CCTTGATTCAGNGTTCCAAGTTTCCCATCCCTGTCATTTTTTAACAGCATGCTGCTTTGG 302

Qy   1521 caa---gttgctgtcactgtttttttcccaggtgttaaaaaaaaaa 1563
          | |    |  |||||||||||||| || || | |   |||||||
Db    303 CCAAGTTTGCTTGTCACTGTTTTTTTTCCCGGGGGTTTNAAAAAAA 348


RESULT  10
H24780/c
LOCUS       H24780        423 bp    mRNA            EST       07-JUL-1995
DEFINITION  yl42g02.s1 Soares breast 3NbHBst Homo sapiens cDNA clone
            IMAGE:160946 3', mRNA sequence.
ACCESSION   H24780
VERSION     H24780.1  GI:893679
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 948
            High quality sequence stops: 318
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 948   Std Error: 0.00
            Seq primer: Promega -21m13
            High quality sequence stop: 318.
FEATURES             Location/Qualifiers
     source          1. .423
                     /organism="Homo sapiens"
                     /db_xref="GDB:575039"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:160946"
                     /clone_lib="Soares breast 3NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
```

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 127 a 85 c 89 g 109 t 13 others
ORIGIN

Query Match 13.1%; Score 262.8; DB 23; Length 423;
Best Local Similarity 94.1%; Pred. No. 1.3e-59;
Matches 301; Conservative 0; Mismatches 15; Indels 4; Gaps 3;

```
Qy   1673 ccaaggaatggagaggaggggaccc--atgtaatccttttgtttagttttgtttttgttt 1730
          |||||||||||| |||||||||||      || |||||||||||||||||||||||||
Db    337 CCAAGGAATGGANAGGAGGGGACCCCATGTAAACCCTTTTGTTTAGTTTTGTTTTTGTTN 278

Qy   1731 tttggtgaatgagaaaggtgtg-ctggtcatggaatggcaggtgtcatatgactgattac 1789
          |||||||||||||||||||| |||||||||||| |||||||||||||||||||| |||
Db    277 TTTGGTGAATGAGAAAGGTGTGCCTGGTCATGGAANGGCAGGTGTCATATGACTGANTAC 218

Qy   1790 tcagagcagatgaggaaaactgtagtctctgagt-cctttgctaatcgcaactcttgtga 1848
          |||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db    217 TCAGAGCAGATGAGGAAAACTGTAGTCTCTGAGTNCCTTTGCTAANCGCAACTCTTGTGA 158

Qy   1849 attattctgattctttttatgcagaatttgattcgtatgatcagtactgactttctgat 1908
          | || ||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Db    157 ANTAATCTGAATCTTTTTTATGCAGAATTTGANTCGTATGATCAGTACTGACTTTCTGAN 98

Qy   1909 tactgtccagcttatagtcttccagtttaatgaactaccatctgatgtttcatatttaag 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 TACTGTCCAGCTTATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAG 38

Qy   1969 tgtatttaaagaaaataaac 1988
          ||||||||||||||||||||
Db     37 TGTATTTAAAGAAAATAAAC 18
```

RESULT 11
H24663/c
LOCUS H24663 272 bp mRNA EST 07-JUL-1995
DEFINITION yl40f12.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160751 3', mRNA sequence.
ACCESSION H24663
VERSION H24663.1 GI:893562
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 272)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 956
High quality sequence stops: 263
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 956 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 263.
FEATURES Location/Qualifiers
source 1. .272
/organism="Homo sapiens"
/db_xref="GDB:574823"
/db_xref="taxon:9606"
/clone="IMAGE:160751"
/clone_lib="Soares breast 3NbHBst"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 85 a 55 c 44 g 75 t 13 others
ORIGIN

Query Match 12.2%; Score 244.6; DB 23; Length 272;
Best Local Similarity 93.6%; Pred. No. 8.5e-55;
Matches 247; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```
Qy   1734 ggtgaatgagaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattactcag 1793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    272 GGTGAATGAGAAAGGTGTGCTGGTCATGGAATGGCAGGTGTCATATGACTGANTACTCAG 213

Qy   1794 agcagatgaggaaaactgtagtctctgagtcctttgctaatcgcaactcttgtgaattat 1853
          |||||| |||| |||||||||| ||||| |||||||||| |||||| | |||||| ||
Db    212 AGCAGANGAGGNAAACTGTAGTCNCTGAGNCCTTTGCTAANCGCAACCCNTGTGAANTAN 153

Qy   1854 tctgattctttttatgcagaatttgattcgtatgatcagtactgactttctgattactg 1913
          |||||||||||||||||||||||| |||||||||||||||||||||||||||| ||||
Db    152 TCTGATTCTTTTTTATGCAGAATTTGNTTCGTATGATCAGTACTGACTTTCTGATNACTG 93

Qy   1914 tccagcttatagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtat 1973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     92 TCCAGCTTATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTAT 33

Qy   1974 ttaaagaaaatаaacaccattatt 1997
          |||||||||| ||||| | |  |
Db     32 TTAAAGAAAATNAACACAAGTTNT 9
```

RESULT 12
AA914687
LOCUS AA914687 474 bp mRNA EST 14-APR-1998
DEFINITION vz03c03.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1314628 5' similar to TR:P97946 P97946 VASCULAR ENDOTHELIAL GROWTH FACTOR D ;, mRNA sequence.
ACCESSION AA914687
VERSION AA914687.1 GI:3054079
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 474)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Sep 29, 1997 this sequence version replaced gi:1520718.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP

```
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:684924
            Putative full length read
            vector to vector length is 637
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 444.
FEATURES              Location/Qualifiers
     source           1. .474
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:1314628"
                      /clone_lib="Soares_mammary_gland_NbMMG"
                      /sex="male"
                      /tissue_type="mammary gland"
                      /dev_stage="4 weeks"
                      /lab_host="DH10B"
                      /note="Organ: mammary gland; Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                      oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of the modified pT7T3 vector.
                      RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                      constructed and normalized by Bento Soares and M.Fatima
                      Bonaldo."
BASE COUNT      127 a     96 c    125 g    125 t      1 others
ORIGIN


  Query Match             10.8%;  Score 217;  DB 40;  Length 474;
  Best Local Similarity   79.0%;  Pred. No. 2.3e-47;
  Matches  289;  Conservative    0;  Mismatches   61;  Indels   16;  Gaps    2;

Qy    340 acaattttctctagctgcctgatgtcaactgcttagtaatcagtggatattg-aaatatt 398
          ||| |||||  |||||||||||    |||||||||||| ||| || || |||  |||||||
Db      1 ACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAGTCATCGGTAGACATTTAAAATATT 60

Qy    399 caaaatgtacagagagtgggtagtggtgaatgttttcatgatgttgtacgtccagctggt 458
          |||||||||  |||| |||| | ||| |||| |  ||||||||||  | ||  |  ||||
Db     61 CAAAATGTATGGAGAATGGGGAATGGGGAATATCCTCATGATGTTCCATGTGTACTTGGT 120

Qy    459 gcagggctccagtaatgaacatggaccagtga--------------agcgatcatctca 503
          ||||||||  |||  |  ||||||||||||||||                ||||||||| |
Db    121 GCAGGGCTTCAGGAGCGAACATGGACCAGTGAAGGATTTTTCTTTTGAGCGATCATCCCG 180

Qy    504 gtccacattggaacgatctgaacagcagatcagggctgcttctagtttggaggaactact 563
          |||||  |||||||||||||||||| |||||| | || ||||||||||||||||||  | ||
Db    181 GTCCATGTTGGAACGATCTGAACAACAGATCCGAGCAGCTTCTAGTTTGGAGGAGTTGCT 240

Qy    564 tcgaattactcactctgaggactggaagctgtggagatgcaggctgaggctcaaaagttt 623
          | |||  | ||||||||||||||||||||||||    ||| || ||| ||||||||||  |
Db    241 GCAAATCGCGCACTCTGAGGACTGGAAGCTGTGGCANTGCTGGTTGAAGCTCAAAAGTCT 300

Qy    624 taccagtatggactctcgctcagcatcccatcggtccactaggtttgcggcaactttcta 683
          | |||||||||||||| ||||||||||||||||| ||||| || ||||||||||||||||
Db    301 TGCCAGTATGGACTCACGCTCAGCATCCCATCGCTCCACCAGATTTGCGGCAACTTTCTA 360

Qy    684 tgacat 689
          |||| |
Db    361 TGACTT 366


RESULT  13
AW259096
LOCUS       AW259096      433 bp    mRNA            EST       23-DEC-1999
DEFINITION  um85h12.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:2331623 5', mRNA sequence.
ACCESSION   AW259096
VERSION     AW259096.1  GI:6632077
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     On May 18, 1998 this sequence version replaced gi:3138242.
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1010827
            Seq primer: custom primer used
            High quality sequence stop: 426.
FEATURES              Location/Qualifiers
     source           1. .433
                      /organism="Mus musculus"
                      /strain="C57BL"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:2331623"
                      /clone_lib="Sugano mouse kidney mkia"
                      /sex="female"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                      (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                      was primed with an oligo(dT) primer
                      [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                      ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                      and cloned into distinct DraIII sites of the pME18S-FL3
                      vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                      be used to isolate the cDNA insert.  Size selection was
                      performed to exclude fragments <1.5kb.  Library
                      constructed by Dr. Sumio Sugano (University of Tokyo
                      Institute of Medical Science).  Custom primers  for
                      sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                      primer CGACCTGCAGCTCGAGCACA."
BASE COUNT      104 a     77 c     90 g    160 t      2 others
ORIGIN


  Query Match             7.6%;  Score 152.8;  DB 79;  Length 433;
  Best Local Similarity   70.2%;  Pred. No. 3.3e-30;
  Matches  281;  Conservative    2;  Mismatches   94;  Indels   23;  Gaps    5;

Qy      3 agctttctgtarctgtaagcattggtggccacaccacctccttacaaagcaactagaacc 62
            ||| | |||||:||| |||  || |||| || |||||||||||| |||||| ||||||||
Db     11 AGCCTGCTGTAACTGCAAGTGTTTGTGGTCATACCACCTCCTTATAAAGCAGCTAGAACC 70

Qy     63 tgcggcatacattggagagatttttt-------aattttctggacaygaagtaaattta 115
          |   || ||   ||| |   |||||||       || |||||||| | ||| |   | ||
Db     71 TTGAGCGTAGGGTGGGGTTTTTTTTTTATCTTCAACTTTCTGGATAAGAAATGTCTGTA 130

Qy    116 gagtgctttcyaatttcaggtagaagacatgtccaccttctgattatttttggag----- 171
          ||||| ||||:| | ||| || ||||| ||| |||||| ||||||||||||| ||
Db    131 GAGTGATTTCTAGTCTCAAGTGGAAGATATGACCACCTCCTGATTATTTTTGCAGCGGGA 190

Qy    171 aacattttgatttttttcatctctctctccccaccctaagattgt-----gcaaaaaaa 225
```

```
          ||| ||   || ||||||||  || ||||||   |    |   |||     |||   |
Db    191 AACTTTGAAATATTTTTCATTGCTTTCTCCCATACTAAGATTGTGTGTGAGGCAGTGAGG 250

Qy    226 gcgtaccttgcctaattgaaataatttcattggattttgatcagaactgatcatttggtt 285
          | || ||||| || | | || | |||||||||||||||| || | ||||||||| || ||
Db    251 GAGTCCCTTGACTTACTCAAGTCATTTCATTGGATTTTAATTACAACTGATCATGTGATT 310

Qy    286 ttctgtgt-----gaagttttgaggtttcaaactttccttctggagaatgccttttgaaa 340
          | | | |     ||  |||| || |||||||||| ||||||||||||||||||| ||
Db    311 GTTTTTTTCCATGTAAAGTTTGGGGCTTCAAACTTTGCTTCTGGAGAATGCCTTTTGCAA 370

Qy    341 caatt-ttctctagctgcctgatgtcaactgcttagtaat 379
          || || |||  ||||||||||    ||||| |||||| ||
Db    371 CACTTNTTCAGTAGCTGCCTGGAAACAACTCCTTAGTCAT 410
```

RESULT 14
AV139144
LOCUS AV139144 288 bp mRNA EST 01-JUL-1999
DEFINITION AV139144 Mus musculus C57BL/6J 10-11 day embryo Mus musculus cDNA clone 2810048M19, mRNA sequence.
ACCESSION AV139144
VERSION AV139144.1 GI:5324874
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 288)
AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs
JOURNAL Unpublished (1999)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3188209.
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .288
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2810048M19"
/clone_lib="Mus musculus C57BL/6J 10-11 day embryo"
/sex="mixed"
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BASE COUNT 77 a 80 c 44 g 87 t
ORIGIN

Query Match 6.1%; Score 121.4; DB 60; Length 288;
Best Local Similarity 79.9%; Pred. No. 7.5e-22;
Matches 143; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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Qy   1164 accagctctctgtgggccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaa 1223
          |||  |||||| | | || ||||| |  ||||| ||| |||  |  |||||  ||| |||
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```
Db      1 ACCCACTCTCTCTCGACCGCACATAACCTTTGATGAAAATCACTTTGAGTGCTTCTTTAA 60

Qy   1224 aacaccatgtcccaaagatctaatccagcaccccaaaaactgcagttgctttgagtgcaa 1283
          | |||||| |||   | |||| || |||||||  |||||| ||||||||||||||||||
Db     61 ACCACCATTTCCGGGAAATCTCATTCAGCACCCGGAAAACTCCAGTTGCTTTGAGTGCAA 120

Qy   1284 agaaagtctggagacctgctgccagaagcacaagctatttcacccagacacctgcagct 1342
          ||||| |||||||| ||||| ||| |||||||||  | ||||||||||||||||||| |
Db    121 AGAAATTCTGGAGAGCTGCTCCCAAAAGCACAAGATTTTTCACCCAGACACCTGCAGGT 179
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RESULT 15
AA458208
LOCUS AA458208 248 bp mRNA EST 06-JUN-1997
DEFINITION vg45g02.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:864338 5', mRNA sequence.
ACCESSION AA458208
VERSION AA458208.1 GI:2180928
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 248)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1288798.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:508426
Putative full length read
vector to vector length is 662
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 241.
FEATURES Location/Qualifiers
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/strain="C57BL/6J"
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/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
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/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 67 a 47 c 66 g 68 t
ORIGIN

Query Match 6.0%; Score 119.6; DB 34; Length 248;

Best Local Similarity 75.2%; Pred. No. 2.2e-21;
Matches 182; Conservative 0; Mismatches 44; Indels 16; Gaps 2;

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          ||| |||||  ||||||||||    ||||||||||| ||| || || ||| |||||||
Db      7 ACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAGTCATCGGTAGACATTTAAAATATT 66

Qy    399 caaaatgtacagagagtgggtagtggtgaatgttttcatgatgttgtacgtccagctggt 458
          |||||||||  |||| |||| | ||| |||| |  |||||||||  | ||  |  ||||
Db     67 CAAAATGTATGGAGAATGGGGAATGGGGAATATCCTCATGATGTTCCATGTGTACTTGGT 126

Qy    459 gcagggctccagtaatgaacatggaccagtga---------------agcgatcatctca 503
          |||||||| ||| |  ||||||||||||||||               |||||||||| |
Db    127 GCAGGGCTTCAGGAGCGAACATGGACCAGTGAAGGATTTTTCTTTTGAGCGATCATCCCG 186

Qy    504 gtccacattggaacgatctgaacagcagatcagggctgcttctagtttggaggaactact 563
          |||||  ||||||||||||||||| |||||| | || ||||||||||||||||  | ||
Db    187 GTCCATGTTGGAACGATCTGAACAACAGATCCGAGCAGCTTCTAGTTTGGAGGAGTTGCT 246

Qy    564 tc 565
            |
Db    247 GC 248
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Search completed: May 16, 2000, 12:32:17
Job time: 3056 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 16, 2000, 12:03:26 ; Search time 1284.53 Seconds
(without alignments)
-1517.656 Million cell updates/sec

Title: US-09-214-982-2
Perfect score: 2004
Sequence: 1 ccagctttctgtarctgtaa.....aaacaccattattcaagtct 2004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
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10: gb_pr2:*
11: gb_pr3:*
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16: gb_vi:*
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18: em_hum1:*
19: em_hum2:*
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33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: em_ba1:*
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43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
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52: gb_htg8:*
53: gb_htg9:*
54: gb_htg10:*
55: gb_htg11:*
56: gb_htg12:*
57: gb_htg13:*
58: gb_htg14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2002.8	99.9	2028	9	D89630	D89630 Homo sapien
2	1998.6	99.7	2029	9	HSAJ185	AJ000185 Homo Sapi
3	1840.8	91.9	1866	10	HSY12863	Y12863 Homo sapien
4	978.6	48.8	1890	5	A61835	A61835 Sequence 1
5	978.6	48.8	1890	12	MMFIGF	X99572 Mus musculu
6	877.2	43.8	1581	12	D89628	D89628 Mus musculu
7	806.6	40.2	1491	12	AF014827	AF014827 Rattus no
8	664.4	33.2	689	10	HSY12870	Y12870 Homo sapien
9	489.2	24.4	1075	10	HSY12864	Y12864 Homo sapien
10	489.2	24.4	39489	11	HSU69570	U69570 Human Xp22
11	215.8	10.8	231	10	HSY12865	Y12865 Homo sapien
12	198.4	9.9	216	10	HSY12869	Y12869 Homo sapien
13	193.8	9.7	211	10	HSY12866	Y12866 Homo sapien
14	151.4	7.6	169	10	HSY12867	Y12867 Homo sapien
15	138.8	6.9	1257	4	CCY15837	Y15837 Coturnix co
16	137.6	6.9	1804	12	MMU58112	U58112 Mus musculu
17	137.6	6.9	1818	12	MMU73620	U73620 Mus musculu
18	130.6	6.5	1939	10	HSU58111	U58111 Human FLT4
19	129	6.4	1997	10	HSVEGFC	X94216 H.sapiens m
20	129	6.4	2015	10	HSU43142	U43142 Human vascu
21	126	6.3	1777	3	AB004275	AB004275 Bos tauru
22	102.4	5.1	121	10	HSY12868	Y12868 Homo sapien
23	65.2	3.3	378	12	AF010302	AF010302 Rattus no
24	53.2	2.7	444	40	AF214570	AF214570 Homo sapi
25	53.2	2.7	541	40	AF091352	AF091352 Homo sapi
26	53.2	2.7	576	5	A64392	A64392 Sequence 5
27	53.2	2.7	576	9	AB021221	AB021221 Homo sapi
28	53.2	2.7	576	11	S82167	S82167 simVEGF165-
29	53.2	2.7	630	9	HSA010438	AJ010438 Homo sapi
30	53.2	2.7	649	10	HSVEGF	X62568 H.sapiens v
31	53.2	2.7	774	5	E13215	E13215 Human mRNA
32	53.2	2.7	774	5	E13332	E13332 cDNA encodi
33	53.2	2.7	774	5	E14233	E14233 Human mRNA
34	53.2	2.7	774	5	E15156	E15156 Human VEGF
35	53.2	2.7	774	24	E11017	E11017 A part of p
36	53.2	2.7	815	11	S85192	S85192 Homo sapien
37	53.2	2.7	990	9	HUMEGFAA	M32977 Human hepar
38	53.2	2.7	1195	9	HUMVPF	M27281 Human vascu
39	53.2	2.7	1649	5	A64396	A64396 Sequence 9
40	53.2	2.7	1664	5	A64404	A64404 Sequence 17
41	53.2	2.7	1787	5	A64394	A64394 Sequence 7
42	53.2	2.7	1790	5	A64398	A64398 Sequence 11
43	53.2	2.7	1790	5	A64400	A64400 Sequence 13
44	53.2	2.7	1832	5	A64402	A64402 Sequence 15
45	53.2	2.7	1873	5	E15157	E15157 Human VEGF

ALIGNMENTS

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D89630
LOCUS       D89630       2028 bp    mRNA            PRI       07-FEB-1999
DEFINITION  Homo sapiens mRNA for VEGF-D, complete cds.
ACCESSION   D89630
VERSION     D89630.1  GI:2780339
KEYWORDS    VEGF-D.
SOURCE      Homo sapiens lung cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2028)
  AUTHORS   Hirata,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-1996) to the DDBJ/EMBL/GenBank databases. Yuichi
            Hirata, Chugai Research Institute for Molecular Medicine, Gene
            search program; 153-2, Nagai, Niihari-Mura, Ibaraki 300-41, Japan
            (E-mail:hiratayu@tk.chugai-pharm.co.jp, Tel:81-298-30-6211,
            Fax:81-298-30-6270)
REFERENCE   2  (sites)
  AUTHORS   Yamada,Y., Nezu,J., Shimane,M. and Hirata,Y.
  TITLE     Molecular cloning of a novel vascular endothelial growth factor,
            VEGF-D
  JOURNAL   Genomics 42 (3), 483-488 (1997)
  MEDLINE   97349118
COMMENT     On Jan 16, 1998 this sequence version replaced gi:2766189.
            Sequence updated (12-Jan-1998).
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ORIGIN
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Qy      61 cctgcggcatacattggagagatttttttaattttctggacaygaagtaaatttagagtg 120
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Qy     121 ctttcyaatttcaggtagaagacatgtccaccttctgattatttttggagaacattttga 180
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Qy     181 ttttttcatctctctctccccaccccctaagattgtgcaaaaaaagcgtaccttgcctaa 240
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Qy     241 ttgaaataatttcattggattttgatcagaactgatcatttggttttctgtgtgaagttt 300
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Qy     301 tgaggtttcaaactttccttctggagaatgccttttgaaacaattttctctagctgcctg 360
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Qy     541 gcttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggaga 600
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Qy     601 tgcaggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtcc 660
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Qy     661 actaggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatgg 720
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Qy     721 caaagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaag 780
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Qy     781 agtaccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgc 840
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Qy     841 aatgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctcttt 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     901 gagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcat 960
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Qy     961 acaggttgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatcc 1020
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Qy    1021 atccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatg 1080
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Qy    1081 ctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaaca 1140
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Qy    1201 gatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaa 1260
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Qy   1921 tatagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtatttaaaga 1980
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Db   1921 TATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTATTTAAAGA 1980

Qy   1981 aaataaacaccattattcaagtct 2004
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Db   1981 AAATAAACACCATTATTCAAGTCT 2004


RESULT   2
HSAJ185
LOCUS       HSAJ185      2029 bp    mRNA            PRI       11-FEB-1998
DEFINITION  Homo Sapiens mRNA for vascular endothelial growth factor-D.
ACCESSION   AJ000185
VERSION     AJ000185.1  GI:2879833
KEYWORDS    vascular endothelial growth factor D; VEGF-D gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2029)
  AUTHORS   Achen,M.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1997) Achen M.G., Angiogenesis Laboratory, Ludwig
            Institute for Cancer Research, Melbourne Tumour Biology Branch,
            Post Office, Royal Melbourne Hospital, Parkville, Victoria 3050,
            AUSTRALIA
REFERENCE   2  (bases 1 to 2029)
  AUTHORS   Achen,M.G., Jeltsch,M., Kukk,E., Makinen,T., Vitali,A., Wilks,A.F.,
            Alitalo,K. and Stacker,S.A.
  TITLE     Vascular endothelial growth factor D (VEGF-D) is a ligand for the
            tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4)
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (2), 548-553 (1998)
  MEDLINE   98118549
FEATURES             Location/Qualifiers
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                     /gene="VEGF-D"
     CDS             411. .1475
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                     ISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHS
                     KKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTP
                     CPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAK
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BASE COUNT      569 a    441 c    435 g    584 t
ORIGIN


  Query Match             99.7%;  Score 1998.6;  DB 9;  Length 2029;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1998;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 ccagctttctgtarctgtaagcattggtggccacaccacctccttacaaagcaactagaa 60
           ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 CCAGCTTTCTGTAGCTGTAAGCATTGGTGGCCACACCACCTCCTTACAAAGCAACTAGAA 68

Qy      61 cctgcggcatacattggagagatttttttaatttttctggacaygaagtaaatttagagtg 120
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Qy     121 ctttcyaatttcaggtagaagacatgtccaccttctgattatttttggagaacattttga 180
           |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     181 ttttttttcatctctctctccccaccctaagattgtgcaaaaaaagcgtaccttgcctaa 240
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Qy     241 ttgaaataatttcattggattttgatcagaactgatcatttggttttctgtgtgaagttt 300
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Qy     301 tgaggtttcaaactttccttctggagaatgccttttgaaacaatttttctctagctgcctg 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     361 atgtcaactgcttagtaatcagtggatattgaaatattcaaaatgtacagagagtgggta 420
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Db     369 ATGTCAACTGCTTAGTAATCAGTGGATATTGAAATATTCAAAATGTACAGAGAGTGGGTA 428

Qy     421 gtggtgaatgttttcatgatgttgtacgtccagctggtgcagggctccagtaatgaacat 480
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Db     429 GTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTGCAGGGCTCCAGTAATGAACAT 488

Qy     481 ggaccagtgaagcgatcatctcagtccacattggaacgatctgaacagcagatcagggct 540
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Qy     541 gcttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggaga 600
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Qy     601 tgcaggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtcc 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     609 TGCAGGCTGAGGCTCAAAAGTTTTACCAGTATGGACTCTCGCTCAGCATCCCATCGGTCC 668

Qy     661 actaggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatgg 720
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Db    669 ACTAGGTTTGCGGCAACTTTCTATGACATTGAAACACTAAAAGTTATAGATGAAGAATGG 728

Qy    721 caaagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaag 780
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Db    729 CAAAGAACTCAGTGCAGCCCTAGAGAAACGTGCGTGGAGGTGGCCAGTGAGCTGGGGAAG 788

Qy    781 agtaccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 AGTACCAACACATTCTTCAAGCCCCCTTGTGTGAACGTGTTCCGATGTGGTGGCTGTTGC 848

Qy    841 aatgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttt 900
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Db    849 AATGAAGAGAGCCTTATCTGTATGAACACCAGCACCTCGTACATTTCCAAACAGCTCTTT 908

Qy    901 gagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcat 960
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Db    909 GAGATATCAGTGCCTTTGACATCAGTACCTGAATTAGTGCCTGTTAAAGTTGCCAATCAT 968

Qy    961 acaggttgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatcc 1020
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Db    969 ACAGGTTGTAAGTGCTTGCCAACAGCCCCCCGCCATCCATACTCAATTATCAGAAGATCC 1028

Qy   1021 atccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatg 1080
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Db   1029 ATCCAGATCCCTGAAGAAGATCGCTGTTCCCATTCCAAGAAACTCTGTCCTATTGACATG 1088

Qy   1081 ctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaaca 1140
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Db   1089 CTATGGGATAGCAACAAATGTAAATGTGTTTTGCAGGAGGAAAATCCACTTGCTGGAACA 1148

Qy   1141 gaagaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaa 1200
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Qy   1201 gatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaa 1260
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Db   1209 GATCGTTGCGAGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAATCCAGCACCCCAAA 1268

Qy   1261 aactgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 AACTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCTGCCAGAAGCACAAGCTA 1328

Qy   1321 tttcacccagacacctgcagctgtgaggacagatgccccctttcataccagaccatgtgca 1380
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Qy   1381 agtggcaaaacagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccag 1440
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Qy   1741 gagaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattactcagagcagat 1800
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Qy   1861 ctttttatgcagaatttgattcgtatgatcagtactgactttctgattactgtccagct 1920
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Qy   1921 tatagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtatttaaaga 1980
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Db   1929 TATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTATTTAAAGA 1988

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Db   1989 AAATAAACACCATTATTCAAGCC 2011
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RESULT   3
HSY12863
LOCUS       HSY12863     1866 bp    mRNA            PRI       02-AUG-1999
DEFINITION  Homo sapiens mRNA for growth factor FIGF.
ACCESSION   Y12863
VERSION     Y12863.1  GI:2909349
KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1866)
  AUTHORS   Rocchigiani,M., Lestingi,M., Luddi,A., Orlandini,M., Franco,B.,
            Rossi,E., Ballabio,A., Zuffardi,O. and Oliviero,S.
  TITLE     Human FIGF: cloning, gene structure, and mapping to chromosome
            Xp22.1 between the PIGA and the GRPR genes
  JOURNAL   Genomics 47 (2), 207-216 (1998)
  MEDLINE   98140120
REFERENCE   2  (bases 1 to 1866)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-1997) S. Oliviero, University of Siena,
            Department of Molecular Biology, Via Fiorentina 1, Siena, 53100,
            ITALY
COMMENT     Related sequence: X99572.
FEATURES             Location/Qualifiers
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BASE COUNT      527 a    407 c    400 g    532 t
ORIGIN
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  Best Local Similarity  99.9%;  Pred. No. 0;
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Db      1 TATTTTTGGAGAACATTTTGATTTTTTTCATCTCTCTCTCCCCACCCCTAAGATTGTGCA 60

Qy    220 aaaaaagcgtaccttgcctaattgaaataatttcattggattttgatcagaactgatcat 279
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Db     61 AAAAAAGCGTACCTTGCCTAATTGAAATAATTTCATTGGATTTTGATCAGAACTGATTAT 120

Qy    280 ttggttttctgtgtgaagttttgaggtttcaaactttccttctggagaatgccttttgaa 339
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Qy    340 acaattttctctagctgcctgatgtcaactgcttagtaatcagtggatattgaaatattc 399
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Db    181 ACAATTTTCTCTAGCTGCCTGATGTCAACTGCTTAGTAATCAGTGGATATTGAAATATTC 240

Qy    400 aaaatgtacagagagtgggtagtggtgaatgttttcatgatgttgtacgtccagctggtg 459
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Db    241 AAAATGTACAGAGAGTGGGTAGTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTG 300

Qy    460 cagggctccagtaatgaacatggaccagtgaagcgatcatctcagtccacattggaacga 519
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Db    301 CAGGGCTCCAGTAATGAACATGGACCAGTGAAGCGATCATCTCAGTCCACATTGGAACGA 360

Qy    520 tctgaacagcagatcagggctgcttctagtttggaggaactacttcgaattactcactct 579
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Db    361 TCTGAACAGCAGATCAGGGCTGCTTCTAGTTTGGAGGAACTACTTCGAATTACTCACTCT 420

Qy    580 gaggactggaagctgtggagatgcaggctgaggctcaaaagttttaccagtatggactct 639
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Db    421 GAGGACTGGAAGCTGTGGAGATGCAGGCTGAGGCTCAAAAGTTTTACCAGTATGGACTCT 480

Qy    640 cgctcagcatcccatcggtccactaggtttgcggcaactttctatgacattgaaacacta 699
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Qy    760 gtggccagtgagctggggaagagtaccaacacattcttcaagccccttgtgtgaacgtg 819
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Qy    820 ttccgatgtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcg 879
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Qy    880 tacatttccaaacagctctttgagatatcagtgcctttgacatcagtacctgaattagtg 939
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Qy    940 cctgttaaagttgccaatcatacaggttgtaagtgcttgccaacagccccccgccatcca 999
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Qy   1000 tactcaattatcagaagatccatccagatccctgaagaagatcgctgttcccattccaag 1059
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Qy   1060 aaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgtgttttgcaggag 1119
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Qy   1120 gaaaatccacttgctggaacagaagaccactctcatctccaggaaccagctctctgtggg 1179
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Qy   1240 gatctaatccagcaccccaaaaactgcagttgctttgagtgcaaagaaagtctggagacc 1299
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Qy   1300 tgctgccagaagcacaagctatttcacccagacacctgcagctgtgaggacagatgcccc 1359
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Qy   1420 aaggagaaaagggctgcccaggggccccacagccgaaagaatccttgattcagcgttcca 1479
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Qy   1540 ttttcccaggtgttaaaaaaaaaaatccattttacacagcaccacagtgaatccagaccaa 1599
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Db   1381 TTTTCCCAGGTGTTAAAAAAAAAATCCATTTTACACAGCACCACAGTGAATCCAGACCAA 1440

Qy   1600 ccttccattcacaccagctaaggagtccctggttcattgatggatgtcttctagctgcag 1659
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Qy   1780 gactgattactcagagcagatgaggaaaactgtagtctctgagtcctttgctaatcgcaa 1839
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Db   1621 GACTGATTACTCAGAGCAGATGAGGAAAACTGTAGTCTCTGAGTCCTTTGCTAATCGCAA 1680

Qy   1840 ctcttgtgaattattctgattctttttttatgcagaatttgattcgtatgatcagtactga 1899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTCTTGTGAATTATTCTGATTCTTTTTTATGCAGAATTTGATTCGTATGATCAGTACTGA 1740

Qy   1900 ctttctgattactgtccagcttatagtcttccagtttaatgaactaccatctgatgtttc 1959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTTTCTGATTACTGTCCAGCTTATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTC 1800

Qy   1960 atatttaagtgtatttaaagaaaataaacaccattattcaagtc 2003
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RESULT   4
A61835
LOCUS       A61835       1890 bp    DNA             PAT       09-MAR-1998
DEFINITION  Sequence 1 from Patent WO9712972.
ACCESSION   A61835
VERSION     A61835.1  GI:3716001
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1890)
  AUTHORS   Oliviero,S.
  TITLE     REGULATED GENES AND USES THEREOF
  JOURNAL   Patent: WO 9712972-A 1 10-APR-1997;
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FEATURES             Location/Qualifiers
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BASE COUNT      510 a    446 c    431 g    503 t
ORIGIN


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          || ||||||   |    |   |||     |||   | | || ||||| || | | || |
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Qy    303 aggtttcaaacttttcctttctggagaatgccttttgaaacaatttttctctagctgcctgat 362
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Qy    587 ggaagctgtggagatgcaggctgaggctcaaaagttttaccagtatggactctcgctcag 646
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Qy    647 catcccatcggtccactaggtttgcggcaactttctatgacattgaaacactaaaagtta 706
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Db    542 CATCCCATCGCTCCACCAGATTTGCGGCAACTTTCTATGACACTGAAACACTAAAAGTTA 601

Qy    707 tagatgaagaatggcaaagaactcagtgcagccctagagaaacgtgcgtggaggtggcca 766
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Db    782 CCAAACAGCTCTTTGAGATATCAGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTA 841

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Qy   1007 ttatcagaagatccatccagatccctgaagaagatcgctgttcccattccaagaaactct 1066
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Db    962 GTCCTATTGACATGCTGTGGGATAACACCAAATGTAAATGTGTTTTGCAAGACGAGACTC 1021

Qy   1127 cacttgctggaacagaagaccactctcatctccaggaaccagctctctgtgggccacaca 1186
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Db   1082 TGACGTTTGATGAAGATCGCTGTGAGTGCGTCTGTAAAGCACCATGTCCGGGAGATCTCA 1141

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Qy   1999 a 1999
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Db   1869 A 1869


RESULT   5
MMFIGF
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DEFINITION  Mus musculus mRNA for new member of PDGF/VEGT family of growth
            factors.
ACCESSION   X99572
VERSION     X99572.1  GI:1695171
KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      house mouse.
  ORGANISM  Mus musculus
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            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1890)
  AUTHORS   Orlandini,M., Marconcini,L., Ferruzzi,R. and Oliviero,S.
  TITLE     Identification of a c-fos-induced gene that is related to the
            platelet-derived growth factor/vascular endothelial growth factor
            family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 93 (21), 11675-11680 (1996)
  MEDLINE   97030254
  REMARK    Erratum:[[published erratum appears in Proc Natl Acad Sci U S A
            1997 Feb 18;94(4):1603]]
REFERENCE   2  (bases 1 to 1890)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUL-1996) S. Oliviero, Universit Degli Studi Di
            Siena, Dipartimento Di Biologia Molecolare, Iris - Via Fiorentina
            1, Siena, 53100, ITALY
COMMENT     Accession number incorrectly cited as U99572 in the publication.
FEATURES             Location/Qualifiers
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BASE COUNT      510 a    446 c    431 g    503 t
ORIGIN


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  Best Local Similarity   74.7%;  Pred. No. 2.1e-239;
  Matches 1435;  Conservative    0;  Mismatches  374;  Indels  112;  Gaps   12;

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Db      2 GAAGATATGACCACCTCCTGATTATTTTTGCAGCGGGAAACTTTGAAATATTTTTCATTG 61

Qy    193 ctctctccccaccccctaagattgt-----gcaaaaaaagcgtaccttgcctaattgaaat 247
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Qy    587 ggaagctgtggagatgcaggctgaggctcaaaagttttaccagtatggactctcgctcag 646
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Qy    827 gtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcgtacattt 886
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Qy    1579 accacagtgaatccagaccaaccttccattcacaccagctaaggagtccctggttcattg 1638

Db    1499 GTCATGGTAAAGCCACATTTCCATGCAATGGCGGCTAGGT---GATTCCCCAGTTCACTG 1555

Qy    1639 atggatgtcttctagctgcagatgcctctgcgcaccaaggaatggagaggaggggaccca 1698

Db    1556 ACAAATGACTTGTAGCTTCAGATGTCTTTGCGCCATCAGCACTCAGAAAGGAAGGGGTCT 1615

Qy    1699 tgtaatccttttgtttagttttgtttttgtttttggtgaatgagaaaggtgtgctggtc 1758

Db    1616 GAGGAGCCCCTTG----------------TTTTGATGAATAAGAAAAGGTTGCCTGAA 1657

Qy    1759 atggaatggcaggtgtcatatgactgattactcagagcagatgaggaaaactgtagtctc 1818

Db    1658 ACAGAGTAGTAGGTGCCACTCGATTGGTTCCTCGGGCTGGCAAAG--------------- 1703

Qy    1819 tgagtcctttgctaatcgcaactcttgtgaattattctgattctttttttatgcagaattt 1878

Db    1703 ----------TCCAAGGGCAATGCTCATGAGTTATTGTGCTTCTTTCTTATGCGGAATTT 1752

Qy    1879 gattcgtatgatcagtactgactttctgattactgtccagcttatagtcttccagtttaa 1938

Db    1753 CATTTGTATGATCAGCACTGA----TCAATTCCCATTCCACTTGTACTTTTTAGGTTTAC 1808

Qy    1939 tgaactaccatctgatgtttcatatttaagtgtatttaaagaaaataaacaccattattc 1998

Db    1809 TGAAGCACTGCCTGATGTTTTATATGTAAATGTATTTAAAGGAAATAAACACTGTTATGC 1868

Qy    1999 a 1999
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Db    1869 A 1869
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RESULT   6
D89628
LOCUS       D89628       1581 bp    mRNA            ROD       07-FEB-1999
DEFINITION  Mus musculus mRNA for vascular endothelial growth factor D,
            complete cds.
ACCESSION   D89628
VERSION     D89628.1  GI:1722697
KEYWORDS    vascular endothelial growth factor D; VEGF-D.
SOURCE      Mus musculus Lung cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1581)
  AUTHORS   Yamada,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-1996) to the DDBJ/EMBL/GenBank databases. Yoshiki
            Yamada, Chugai Research Institute for Molecular Medicine, Gene
            search program; 153-2,Nagai, Niihari-mura, Ibaraki 300-41, Japan
            (E-mail:yamaday@tk.chugai-pharm.co.jp, Tel:81-298-30-6211,
            Fax:81-298-30-6270)
REFERENCE   2  (sites)
  AUTHORS   Yamada,Y., Nezu,J., Shimane,M. and Hirata,Y.
  TITLE     Molecular cloning of a novel vascular endothelial growth factor,
            VEGF-D
  JOURNAL   Genomics 42 (3), 483-488 (1997)
  MEDLINE   97349118
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     source          1. .1581
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                     /tissue_type="Lung"
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                     /gene="VEGF-D"
     CDS             96. .1172
                     /gene="VEGF-D"
                     /codon_start=1
                     /product="vascular endothelial growth factor D"
                     /protein_id="BAA14002.1"
                     /db_xref="GI:1722698"
                     /translation="MYGEWGMGNILMMFHVYLVQGFRSEHGPVKDFSFERSSRSMLER
                     SEQQIRAASSLEELLQIAHSEDWKLWRCRLKLKSLASMDSRSASHRSTRFAATFYDTE
                     TLKVIDEEWQRTQCSPRETCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEEGVMCMN
                     TSTSYISKQLFEISVPLTSVPELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQTPEED
                     ECPHSKKLCPIDMLWDNTKCKCVLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCEC
                     VCKAPCPGDLIQHPENCSCFECKESLESCCQKHKIFHPDTCSCEDRCPFHTRTCASRK
                     PACGKHWRFPKETRAQGLYSQENP"
BASE COUNT      420 a    401 c    367 g    392 t      1 others
ORIGIN
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  Query Match           43.8%;  Score 877.2;  DB 12;  Length 1581;
  Best Local Similarity  84.2%;  Pred. No. 1.6e-213;
  Matches 1044;  Conservative    0;  Mismatches  173;  Indels   23;  Gaps    4;

Qy     319 ttctggagaatgccttttgaaacaattttctctagctgcctgatgtcaactgcttagtaa 378

Db      11 TGCTGGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAGTCA 70

Qy     379 tcagtggata-ttgaaatattcaaaatgtacagagagtgggtagtggtgaatgttttcat 437

Db      71 TCGGTAGACATTTAAAATATTCAAAATGTATGGAGAATGGGGAATGGGGAATATCCTCAT 130

Qy     438 gatgttgtacgtccagctggtgcagggctccagtaatgaacatggaccagtga------- 491

Db     131 GATGTTCCATGTGTACTTGGTGCAGGGCTTCAGGAGCGAACATGGACCAGTGAAGGATTT 190

Qy     491 --------agcgatcatctcagtccacattggaacgatctgaacagcagatcagggctgc 542

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Qy     543 ttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggagatg 602

Db     251 TTCTAGTTTGGAGGAGTTGCTGCAAATCGCGCACTCTGAGGACTGGAAGCTGTGGCGATG 310

Qy     603 caggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtccac 662

Db     311 CCGGTTGAAGCTCAAAAGTCTTGCCAGTATGGACTCACGCTCAGCATCCCATCGCTCCAC 370

Qy     663 taggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatggca 722

Db     371 CAGATTTGCGGCAACTTTCTATGACACTGAAACACTAAAAGTTATAGATGAAGAATGGCA 430

Qy     723 aagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaagag 782

Db     431 GAGGACCCAATGCAGCCCTAGAGAGACATGCGTAGAAGTCGCCAGTGAGCTGGGGAAGAC 490

Qy     783 taccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgcaa 842

Db     491 AACCAACACATTCTTCAAGCCCCCCTGTGTAAATGTCTTCCGGTGTGGAGGCTGCTGCAA 550

Qy     843 tgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttga 902

Db     551 CGAAGAGGGTGTGATGTGTATGAACACAAGCACCTCCTACATCTCCAAACAGCTCTTTGA 610

Qy     903 gatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcatac 962
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Db    611 GATATCAGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTAAAATTGCCAACCATAC 670

Qy    963 aggttgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatccat 1022
Db    671 GGGTTGTAAGTGCTTGCCCACGGGCCCCCGCCATCCTTACTCAATTATCAGAAGATCCAT 730

Qy   1023 ccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatgct 1082
Db    731 TCAGACCCCAGAAGAAGATGAATGTCCTCATTCCAAGAAACTCTGTCCTATTGACATGCT 790

Qy   1083 atgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaacaga 1142
Db    791 GTGGGATAACACCAAATGTAAATGTGTTTTGCAAGACGAGACTCCACTGCCTGGGACAGA 850

Qy   1143 agaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaaga 1202
Db    851 AGACCACTCTTACCTCCAGGAACCCACTCTCTGTGGACCGCACATGACGTTTGATGAAGA 910

Qy   1203 tcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaaaa 1262
Db    911 TCGCTGTGAGTGCGTCTGTAAAGCACCATGTCCGGGAGATCTCATTCAGCACCCGGAAAA 970

Qy   1263 ctgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagctatt 1322
Db    971 CTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGAGCTGCTGCCAAAAGCACAAGATTTT 1030

Qy   1323 tcacccagacacctgcagctgtgaggacagatgccccttttcataccagaccatgtgcaag 1382
Db   1031 TCACCCAGACACCTGCAGCTGTGAGGACAGATGTCCTTTTCACACCAGAACATGTGCAAG 1090

Qy   1383 tggcaaaacagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccaggg 1442
Db   1091 TAGAAAGCCAGCCTGTGGAAAGCACTGGCGCTTTCCAAAGGAGACAAGG---GCCCAGGG 1147

Qy   1443 gccccacagccgaaagaatccttgattca----gcgttccaagttccccatccctgtcat 1498
Db   1148 ACTCTACAGCCAGGAGAACCCTTGATTCAACTTCCTTTCAAGTCCCCCCATCTCTGTCAT 1207

Qy   1499 ttttaacagcatgctgctttgccaagttgctgtcactgtt 1538
Db   1208 TTTAAACAGCTCACTGCTTTGTCAAGTTGCTGTCACTGTT 1247
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RESULT   7
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LOCUS       AF014827     1491 bp    mRNA            ROD       12-AUG-1997
DEFINITION  Rattus norvegicus vascular endothelial growth factor D (VEGF-D)
            mRNA, complete cds.
ACCESSION   AF014827
VERSION     AF014827.1  GI:2323338
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1491)
  AUTHORS   Yamada,Y., Nezu,J., Shimane,M. and Hirata,Y.
  TITLE     Molecular cloning of a novel vascular endothelial growth factor,
            VEGF-D
  JOURNAL   Genomics 42 (3), 483-488 (1997)
  MEDLINE   97349118
REFERENCE   2  (bases 1 to 1491)
  AUTHORS   Yamada,Y., Hirata,Y., Nezu,J. and Shimane,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUL-1997) Gene Search Program, Chugai Research
            Institute for Molecular Medicine, 153-2 NAGAI NIIHARI, Ibaraki
            300-41, Japan
FEATURES             Location/Qualifiers
     source          1. .1491
                     /organism="Rattus norvegicus"
                     /strain="Sprague Dawley"
                     /db_xref="taxon:10116"
     gene            1. .1491
                     /gene="VEGF-D"
     CDS             270. .1250
                     /gene="VEGF-D"
                     /codon_start=1
                     /product="vascular endothelial growth factor D"
                     /protein_id="AAB66557.1"
                     /db_xref="GI:2323339"
                     /translation="MYGEWAAVNILMMSYVYLVQGFSIEHRAVKDVSLERSSRSVLER
                     SEQQIRAASTLEELLQVAHSEDWKLWRCRLKLKSLANVDSRSTSHRSTRFAATFYDTE
                     TLKVIDEEWQRTQCSPRETCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEESVMCMN
                     TSTSYISKQLFEISVPLTSVPELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQIPEED
                     QCPHSKKLCPVDMLWDNTKCKCVLQDENPLPGTEDHSYLQEPALCGPHMMFDEDRCEC
                     VCKAPCPGDLIQHPENCSCFECKESLESCCQKHKMFHPDTCRSMVFSLSP"
BASE COUNT      399 a    336 c    339 g    417 t
ORIGIN
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  Query Match           40.2%;  Score 806.6;  DB 12;  Length 1491;
  Best Local Similarity  81.6%;  Pred. No. 1.7e-195;
  Matches 1004;  Conservative    0;  Mismatches  199;  Indels   28;  Gaps    5;

Qy    148 ccaccttctgattatttttggag-----aacattttgatttttttcatctctctctcccc 202
Db      2 CCACCTCTTGATTATTTGTGCAGCGGGAAACTTTGAAATAGTTTTCATCTCTTTCTCCCA 61

Qy    203 acccctaagattgtgcaaaaaaagcgta--ccttgcctaattgaaataatttcattggat 260
Db     62 TACTAAGATTGTGTGTGGCCGTGGGGGAGTCCTTGACTAACTCAAGTCATTTCATTGGAT 121

Qy    261 tttgatcagaactgatcatttgg-----ttttctgtgtgaagttttgaggtttcaaactt 315
Db    122 TTTGATTACAACTGATCATGTGATATTTTTTTCCATGTAAAGTTTTGGGGCTTCAAACTT 181

Qy    316 tccttctggagaatgccttttgaaacaattttctctagctgcctgatgtcaactgcttag 375
Db    182 TGCTTCTGGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAG 241

Qy    376 taatcagtggata-ttgaaatattcaaaatgtacagagagtgggtagtggtgaatgtttt 434
Db    242 CCATCAGTGGACATTTGAAATATTCAAAATGTATGGAGAGTGGGCCGCAGTGAATATTCT 301

Qy    435 catgatgttgtacgtccagctggtgcagggctccagtaatgaacatggaccagtga---- 491
Db    302 CATGATGTCCTATGTGTACCTGGTGCAGGGCTTCAGTATTGAACACCGAGCAGTGAAGGA 361

Qy    491 ----------agcgatcatctcagtccacattggaacgatctgaacagcagatcagggc 539
Db    362 TGTTTCTCTTGAGCGATCATCCCGGTCTGTGTTGGAACGTTCTGAACAACAGATCCGCGC 421

Qy    540 tgcttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggag 599
Db    422 GGCTTCTACTTTGGAAGAGTTGCTGCAAGTCGCACACTCTGAGGACTGGAAGCTGTGGCG 481

Qy    600 atgcaggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtc 659
Db    482 GTGCCGGTTGAAGCTTAAAAGTCTTGCCAATGTGGACTCGCGCTCAACATCCCATCGCTC 541

Qy    660 cactaggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatg 719
Db    542 CACCAGATTTGCGGCAACTTTCTATGATACTGAAACACTAAAAGTTATAGATGAAGAATG 601

Qy    720 gcaaagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaa 779
Db    602 GCAGAGGACCCAATGCAGCCCTAGAGAGACATGCGTAGAAGTCGCCAGTGAGCTGGGGAA 661

Qy    780 gagtaccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttg 839
Db    662 GACAACCAACACATTTTTCAAGCCCCCTTGTGTAAATGTCTTCCGGTGTGGAGGATGCTG 721

Qy    840 caatgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctt 899
Db    722 CAATGAAGAGAGCGTGATGTGTATGAACACAAGCACCTCCTACATCTCCAAACAGCTCTT 781
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Qy     900 tgagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatca 959
           |||||||||||||||| ||||||||| || || |||||||||||||| ||||||| ||
Db     782 TGAGATATCAGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTAAAATTGCCAACCA 841

Qy     960 tacaggttgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatc 1019
           ||| |||||||||||| ||||| || | |||||| ||||| || ||||||||||||||||
Db     842 TACGGGTTGTAAGTGTTTGCCCACGGGCCCCCGGCATCCTTATTCAATTATCAGAAGATC 901

Qy    1020 catccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacat 1079
           ||| |||||||| |||||||||  ||| | |||||||||||||||||||| |||||||
Db     902 CATTCAGATCCCAGAAGAAGATCAATGTCCTCATTCCAAGAAACTCTGTCCTGTTGACAT 961

Qy    1080 gctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaac 1139
           ||| ||||||| || |||||||||||||||||| || || || ||||||||  |||| ||
Db     962 GCTGTGGGATAACACCAAATGTAAATGTGTTTTACAAGATGAGAATCCACTGCCTGGGAC 1021

Qy    1140 agaagaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacga 1199
           |||||||||||||| | |||||||||||| |||||||||| ||||||||||||||||| ||
Db    1022 AGAAGACCACTCTTACCTCCAGGAACCCGCTCTCTGTGGACCACACATGATGTTTGATGA 1081

Qy.   1200 agatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaa 1259
           |||||| |||||||||||||||||| |||||||||   |||||| || ||||||||  |
Db    1082 AGATCGCTGCGAGTGTGTCTGTAAAGCACCATGTCCTGGAGATCTCATTCAGCACCCGGA 1141

Qy    1260 aaactgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagct 1319
           |||||||||||||||||| |||||||||||||||| | ||| ||||| |||||||| |
Db    1142 AAACTGCAGTTGCTTTGAATGCAAAGAAAGTCTGGAAAGCTGTTGCCAAAAGCACAAGAT 1201

Qy    1320 atttcacccagacacctgcagctgtgaggac 1350
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Db    1202 GTTTCACCCTGACACCTGCAGATCAATGGTC 1232
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RESULT   8
HSY12870
LOCUS       HSY12870      689 bp    DNA             PRI       02-AUG-1999
DEFINITION  Homo sapiens FIGF gene, exon 7.
ACCESSION   Y12870
VERSION     Y12870.1  GI:2909358
KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Rocchigiani,M., Lestingi,M., Luddi,A., Orlandini,M., Franco,B.,
            Rossi,E., Ballabio,A., Zuffardi,O. and Oliviero,S.
  TITLE     Human FIGF: cloning, gene structure, and mapping to chromosome
            Xp22.1 between the PIGA and the GRPR genes
  JOURNAL   Genomics 47 (2), 207-216 (1998)
  MEDLINE   98140120
REFERENCE   2  (bases 1 to 689)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) S. Oliviero, University of Siena,
            Department of Molecular Biology, Via Fiorentina 1, Siena, 53100,
            ITALY
COMMENT     Related sequence: X99572.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="p22.2"
                     /dev_stage="adult"
     gene            11. .679
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                     /gene="FIGF"
                     /number=7
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ORIGIN


  Query Match             33.2%;  Score 664.4;  DB 10;  Length 689;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-159;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1338 cagctgtgaggacagatgccccttttcataccagaccatgtgcaagtggcaaaacagcatg 1397
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Db       8 CAGCTGTGAGGACAGATGCCCCTTTCATACCAGACCATGTGCAAGTGGCAAAACAGCATG 67

Qy    1398 tgcaaagcattgccgctttccaaaggagaaaagggctgcccaggggccccacagccgaaa 1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68 TGCAAAGCATTGCCGCTTTCCAAAGGAGAAAAGGGCTGCCCAGGGGCCCCACAGCCGAAA 127

Qy    1458 gaatccttgattcagcgttccaagttccccatccctgtcatttttaacagcatgctgctt 1517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     128 GAATCCTTGATTCAGCGTTCCAAGTTCCCCATCCCTGTCATTTTTAACAGCATGCTGCTT 187

Qy    1518 tgccaagttgctgtcactgtttttttcccaggtgttaaaaaaaaaatccattttacacag 1577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     188 TGCCAAGTTGCTGTCACTGTTTTTTTCCCAGGTGTTAAAAAAAAAATCCATTTTACACAG 247

Qy    1578 caccacagtgaatccagaccaaccttccattcacaccagctaaggagtccctggttcatt 1637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     248 CACCACAGTGAATCCAGACCAACCTTCCATTCACACCAGCTAAGGAGTCCCTGGTTCATT 307

Qy    1638 gatggatgtcttctagctgcagatgcctctgcgcaccaaggaatggagaggaggggaccc 1697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 GATGGATGTCTTCTAGCTGCAGATGCCTCTGCGCACCAAGGAATGGAGAGGAGGGGACCC 367

Qy    1698 atgtaatccttttgtttagttttgtttttgttttttggtgaatgagaaaggtgtgctggt 1757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 ATGTAATCCTTTTGTTTAGTTTTGTTTTTGTTTTTTGGTGAATGAGAAAGGTGTGCTGGT 427

Qy    1758 catggaatggcaggtgtcatatgactgattactcagagcagatgaggaaaactgtagtct 1817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 CATGGAATGGCAGGTGTCATATGACTGATTACTCAGAGCAGATGAGGAAAACTGTAGTCT 487

Qy    1818 ctgagtcctttgctaatcgcaactcttgtgaattattctgattctttttttatgcagaatt 1877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     488 CTGAGTCCTTTGCTAATCGCAACTCTTGTGAATTATTCTGATTCTTTTTTTATGCAGAATT 547

Qy    1878 tgattcgtatgatcagtactgactttctgattactgtccagcttatagtcttccagttta 1937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     548 TGATTCGTATGATCAGTACTGACTTTCTGATTACTGTCCAGCTTATAGTCTTCCAGTTTA 607

Qy    1938 atgaactaccatctgatgtttcatatttaagtgtatttaaagaaaataaacaccattatt 1997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1998 caagtc 2003
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Db     668 CAAGCC 673
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RESULT   9
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LOCUS       HSY12864      1075 bp    DNA             PRI       02-AUG-1999
DEFINITION  Homo sapiens FIGF gene, promoter exon 1 and joined CDS.
ACCESSION   Y12864
VERSION     Y12864.1  GI:2909351
KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1075)
  AUTHORS   Rocchigiani,M., Lestingi,M., Luddi,A., Orlandini,M., Franco,B.,
            Rossi,E., Ballabio,A., Zuffardi,O. and Oliviero,S.
  TITLE     Human FIGF: cloning, gene structure, and mapping to chromosome
            Xp22.1 between the PIGA and the GRPR genes
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  JOURNAL   Genomics 47 (2), 207-216 (1998)
  MEDLINE   98140120
REFERENCE   2  (bases 1 to 1075)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-1997) S. Oliviero, University of Siena,
            Department of Molecular Biology, Via Fiorentina 1, Siena, 53100,
            ITALY
COMMENT     Related sequence: X99572.
FEATURES             Location/Qualifiers
     source          1. .1075
                     /organism="Homo sapiens"
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                     /chromosome="X"
                     /map="p22.2"
                     /dev_stage="adult"
     promoter        1. .465
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                     Y12867.1:11. .159,Y12868.1:11. .111,Y12869.1:11. .206,
                     Y12870.1:11. .679)
                     /label=FIGFmRNA
     exon            467. .1065
                     /number=1
     gene            join(976. .1065,Y12865.1:11. .221,Y12866.1:11. .201,
                     Y12867.1:11. .159,Y12868.1:11. .111,Y12869.1:11. .206,
                     Y12870.1:11. .137)
                     /gene="FIGF"
     CDS             join(976. .1065,Y12865.1:11. .221,Y12866.1:11. .201,
                     Y12867.1:11. .159,Y12868.1:11. .111,Y12869.1:11. .206,
                     Y12870.1:11. .137)
                     /gene="FIGF"
                     /codon_start=1
                     /label=FIGFCDS
                     /product="growth factor FIGF"
                     /protein_id="CAA73371.1"
                     /db_xref="GI:2909352"
                     /db_xref="SPTREMBL:O43915"
                     /translation="MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQI
                     RAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVI
                     DEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSY
                     ISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHS
                     KKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTP
                     CPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAK
                     HCRFPKEKRAAQGPHSRKNP"
BASE COUNT      289 a    189 c    220 g    377 t
ORIGIN


  Query Match             24.4%;  Score 489.2;  DB 10;  Length 1075;
  Best Local Similarity   99.2%;  Pred. No. 2e-114;
  Matches  488;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ccagctttctgtarctgtaagcattggtggccacaccacctccttacaaagcaactagaa 60
           |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db     574 CCAGCTTTCTGTAGCTGTAAGCATTGGTGGCCACACCACCTCCTTACAAAGCAACTAGAA 633

Qy      61 cctgcggcatacattggagagatttttttaattttctggacaygaagtaaatttagagtg 120
           ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db     634 CCTGCGGCATACATTGGAGAGATTTTTTTAATTTTCTGGACATGAAGTAAATTTAGAGTG 693

Qy     121 ctttcyaatttcaggtagaagacatgtccaccttctgattatttttggagaacattttga 180
           |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 CTTTCTAATTTCAGGTAGAAGACATGTCCACCTTCTGATTATTTTTGGAGAACATTTTGA 753

Qy     181 ttttttttcatctctctctccccaccccctaagattgtgcaaaaaaagcgtaccttgcctaa 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 TTTTTTTCATCTCTCTCTCCCCACCCCTAAGATTGTGCAAAAAAAGCGTACCTTGCCTAA 813

Qy     241 ttgaaataatttcattggattttgatcagaactgatcatttggttttctgtgtgaagttt 300
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     814 TTGAAATAATTTCATTGGATTTTGATCAGAACTGATTATTTGGTTTTCTGTGTGAAGTTT 873

Qy     301 tgaggtttcaaactttccttctggagaatgccttttgaaacaattttctctagctgcctg 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 TGAGGTTTCAAACTTTCCTTCTGGAGAATGCCTTTTGAAACAATTTTCTCTAGCTGCCTG 933

Qy     361 atgtcaactgcttagtaatcagtggatattgaaatattcaaaatgtacagagagtgggta 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 ATGTCAACTGCTTAGTAATCAGTGGATATTGAAATATTCAAAATGTACAGAGAGTGGGTA 993

Qy     421 gtggtgaatgttttcatgatgttgtacgtccagctggtgcagggctccagtaatgaacat 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994 GTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTGCAGGGCTCCAGTAATGAACAT 1053

Qy     481 ggaccagtgaag 492
           ||||||||||||
Db    1054 GGACCAGTGAAG 1065


RESULT  10
HSU69570
LOCUS       HSU69570    39489 bp    DNA             PRI       07-FEB-1997
DEFINITION  Human Xp22 cosmid U27H1, complete sequence.
ACCESSION   U69570
VERSION     U69570.1  GI:1825473
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39489)
  AUTHORS   Lu,J. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-SEP-1996) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Feb 7, 1997 this sequence version replaced gi:1552535.
FEATURES             Location/Qualifiers
     source          1. .39489
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xp22"
                     /clone="10E6"
                     /clone_lib="LLNL X chromosome library LL0XNC01"
     repeat_region   350. .798
                     /rpt_family="L1MA2"
     repeat_region   420. .608
                     /rpt_family="L1MA10"
     repeat_region   complement(955. .1110)
                     /rpt_family="Alu"
     repeat_region   1834. .2117
                     /rpt_family="Alu"
     repeat_region   2147. .2419
                     /rpt_family="Alu"
     STS             4404. .4573
                     /db_xref="dbSTS:G02051"
     repeat_region   complement(4928. .5080)
                     /rpt_family="L1"
     misc_feature    5642. .5731
                     /note="similar to ESTs with GenBank Accession Numbers
                     W27937 and N29255"
                     /note="Region: 39g10"
                     /db_xref="dbEST:W27937"
                     /db_xref="dbEST:N29255"
     repeat_region   6140. .6427
                     /rpt_family="Alu"
     repeat_region   7504. .7578
                     /rpt_family="MIR"
     repeat_region   complement(9106. .9726)
                     /rpt_family="MER1A"
     repeat_region   complement(10925. .10987)
                     /rpt_family="MLT1f"
     misc_feature    12926. .12996
                     /note="similar to ESTs with GenBank Accession Numbers
                     W27937, W29126, N20542."
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                  /note="Region: 39g10"
     repeat_region   complement(14647. .14754)
                  /rpt_family="MIR"
     repeat_region   15217. .15311
                  /rpt_family="MER5"
     repeat_region   15783. .16080
                  /rpt_family="Alu"
     misc_feature    17660. .17899
                  /note="similar to EST with GenBank Accession Number
                  N47571"
                  /note="Region: yy91f09.r1"
     misc_feature    17958. .18376
                  /note="similar to ESTs with GenBank Accession Numbers
                  W29126, N47571, W27937 and N20542"
                  /note="Region: yy91f09.s1"
     repeat_region   complement(20857. .21139)
                  /rpt_family="Alu"
     repeat_region   complement(28438. .29040)
                  /rpt_family="L1ME2"
     repeat_region   32018. .32074
                  /rpt_family="MER5"
     repeat_region   complement(33579. .33732)
                  /rpt_family="L1MD1"
     repeat_region   complement(35236. .35487)
                  /rpt_family="Alu"
     repeat_region   36873. .37150
                  /rpt_family="Alu"
     repeat_region   37761. .38007
                  /rpt_family="Alu"
     repeat_region   complement(39161. .39489)
                  /rpt_family="MLT1b"
BASE COUNT    12027 a   7669 c   7510 g  12283 t
ORIGIN


  Query Match             24.4%;  Score 489.2;  DB 11;  Length 39489;
  Best Local Similarity   99.2%;  Pred. No. 1.9e-114;
  Matches  488;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ccagctttctgtarctgtaagcattggtggccacaccacctccttacaaagcaactagaa 60
          ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db  18831 CCAGCTTTCTGTAGCTGTAAGCATTGGTGGCCACACCACCTCCTTACAAAGCAACTAGAA 18890

Qy     61 cctgcggcatacattggagagatttttttaattttctggacaygaagtaaatttagagtg 120
          ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db  18891 CCTGCGGCATACATTGGAGAGATTTTTTTAATTTTCTGGACATGAAGTAAATTTAGAGTG 18950

Qy    121 ctttcyaatttcaggtagaagacatgtccaccttctgattatttttggagaacattttga 180
          |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18951 CTTTCTAATTTCAGGTAGAAGACATGTCCACCTTCTGATTATTTTTGGAGAACATTTTGA 19010

Qy    181 ttttttttcatctctctctccccaccccctaagattgtgcaaaaaaagcgtaccttgcctaa 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19011 TTTTTTTCATCTCTCTCTCCCCACCCCTAAGATTGTGCAAAAAAAGCGTACCTTGCCTAA 19070

Qy    241 ttgaaataatttcattggattttgatcagaactgatcatttggttttctgtgtgaagttt 300
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  19071 TTGAAATAATTTCATTGGATTTTGATCAGAACTGATTATTTGGTTTTCTGTGTGAAGTTT 19130

Qy    301 tgaggtttcaaactttccttctggagaatgccttttgaaacaattttctctagctgcctg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19131 TGAGGTTTCAAACTTTCCTTCTGGAGAATGCCTTTTGAAACAATTTTCTCTAGCTGCCTG 19190

Qy    361 atgtcaactgcttagtaatcagtggatattgaaatattcaaaatgtacagagagtgggta 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19191 ATGTCAACTGCTTAGTAATCAGTGGATATTGAAATATTCAAAATGTACAGAGAGTGGGTA 19250

Qy    421 gtggtgaatgttttcatgatgttgtacgtccagctggtgcagggctccagtaatgaacat 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19251 GTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTGCAGGGCTCCAGTAATGAACAT 19310

Qy  481 ggaccagtgaag 492
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Db  19311 GGACCAGTGAAG 19322


RESULT  11
HSY12865
LOCUS       HSY12865      231 bp    DNA             PRI       02-AUG-1999
DEFINITION  Homo sapiens FIGF gene, exon 2.
ACCESSION   Y12865
VERSION     Y12865.1  GI:2909353
KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 231)
  AUTHORS   Rocchigiani,M., Lestingi,M., Luddi,A., Orlandini,M., Franco,B.,
            Rossi,E., Ballabio,A., Zuffardi,O. and Oliviero,S.
  TITLE     Human FIGF: cloning, gene structure, and mapping to chromosome
            Xp22.1 between the PIGA and the GRPR genes
  JOURNAL   Genomics 47 (2), 207-216 (1998)
  MEDLINE   98140120
REFERENCE   2  (bases 1 to 231)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-1997) S. Oliviero, University of Siena,
            Department of Molecular Biology, Via Fiorentina 1, Siena, 53100,
            ITALY
COMMENT     Related sequence: X99572.
FEATURES             Location/Qualifiers
     source          1. .231
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="p22.2"
                     /dev_stage="adult"
     gene            11. .221
                     /gene="FIGF"
     exon            11. .221
                     /gene="FIGF"
                     /number=2
                     /usedin=Y12864:FIGFCDS
                     /usedin=Y12864:FIGFmRNA
BASE COUNT       60 a     50 c     56 g     65 t
ORIGIN


  Query Match             10.8%;  Score 215.8;  DB 10;  Length 231;
  Best Local Similarity   99.1%;  Pred. No. 1.3e-44;
  Matches  217;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    488 tgaagcgatcatctcagtccacattggaacgatctgaacagcagatcagggctgcttcta 547
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 TTAAGCGATCATCTCAGTCCACATTGGAACGATCTGAACAGCAGATCAGGGCTGCTTCTA 65

Qy    548 gtttggaggaactacttcgaattactcactctgaggactggaagctgtggagatgcaggc 607
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 GTTTGGAGGAACTACTTCGAATTACTCACTCTGAGGACTGGAAGCTGTGGAGATGCAGGC 125

Qy    608 tgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtccactaggt 667
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 TGAGGCTCAAAAGTTTTACCAGTATGGACTCTCGCTCAGCATCCCATCGGTCCACTAGGT 185

Qy    668 ttgcggcaactttctatgacattgaaacactaaaagtta 706
          ||||||||||||||||||||||||||||||||||| ||
Db    186 TTGCGGCAACTTTCTATGACATTGAAACACTAAAAGGTA 224


RESULT  12
HSY12869
LOCUS       HSY12869      216 bp    DNA             PRI       02-AUG-1999
DEFINITION  Homo sapiens FIGF gene, exon 6.
ACCESSION   Y12869
VERSION     Y12869.1  GI:2909357
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KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 216)
  AUTHORS   Rocchigiani,M., Lestingi,M., Luddi,A., Orlandini,M., Franco,B.,
            Rossi,E., Ballabio,A., Zuffardi,O. and Oliviero,S.
  TITLE     Human FIGF: cloning, gene structure, and mapping to chromosome
            Xp22.1 between the PIGA and the GRPR genes
  JOURNAL   Genomics 47 (2), 207-216 (1998)
  MEDLINE   98140120
REFERENCE   2  (bases 1 to 216)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) S. Oliviero, University of Siena,
            Department of Molecular Biology, Via Fiorentina 1, Siena, 53100,
            ITALY
COMMENT     Related sequence: X99572.
FEATURES             Location/Qualifiers
     source          1. .216
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="p22.2"
                     /dev_stage="adult"
     gene            11. .206
                     /gene="FIGF"
     exon            11. .206
                     /gene="FIGF"
                     /number=6
                     /usedin=Y12864:FIGFCDS
                     /usedin=Y12864:FIGFmRNA
BASE COUNT       61 a     60 c     44 g     51 t
ORIGIN
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  Query Match             9.9%;  Score 198.4;  DB 10;  Length 216;
  Best Local Similarity   99.5%;  Pred. No. 3.6e-40;
  Matches  199;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1143 agaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaaga 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 AGACCACTCTCATCTCCAGGAACCAGCTCTCTGTGGGCCACACATGATGTTTGACGAAGA 68

Qy   1203 tcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaaaa 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 TCGTTGCGAGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAATCCAGCACCCCAAAAA 128

Qy   1263 ctgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagctatt 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 CTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCTGCCAGAAGCACAAGCTATT 188

Qy   1323 tcacccagacacctgcagct 1342
          ||||||||||||||||||| |
Db    189 TCACCCAGACACCTGCAGGT 208
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RESULT  13
HSY12866
LOCUS       HSY12866      211 bp    DNA             PRI       02-AUG-1999
DEFINITION  Homo sapiens FIGF gene, exon 3.
ACCESSION   Y12866
VERSION     Y12866.1  GI:2909354
KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 211)
  AUTHORS   Rocchigiani,M., Lestingi,M., Luddi,A., Orlandini,M., Franco,B.,
            Rossi,E., Ballabio,A., Zuffardi,O. and Oliviero,S.
  TITLE     Human FIGF: cloning, gene structure, and mapping to chromosome
            Xp22.1 between the PIGA and the GRPR genes
  JOURNAL   Genomics 47 (2), 207-216 (1998)
  MEDLINE   98140120
REFERENCE   2  (bases 1 to 211)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) S. Oliviero, University of Siena,
            Department of Molecular Biology, Via Fiorentina 1, Siena, 53100,
            ITALY
COMMENT     Related sequence: X99572.
FEATURES             Location/Qualifiers
     source          1. .211
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="p22.2"
                     /dev_stage="adult"
     gene            11. .201
                     /gene="FIGF"
     exon            11. .201
                     /gene="FIGF"
                     /number=3
                     /usedin=Y12864:FIGFCDS
                     /usedin=Y12864:FIGFmRNA
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ORIGIN
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  Best Local Similarity   99.0%;  Pred. No. 5.4e-39;
  Matches  195;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    702 agttatagatgaagaatggcaaagaaactcagtgcagccctagagaaacgtgcgtggaggt 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 AGTTATAGATGAAGAATGGCAAAGAACTCAGTGCAGCCCTAGAGAAACGTGCGTGGAGGT 68

Qy    762 ggccagtgagctggggaagagtaccaacacattcttcaagccccctgtgtgaacgtgtt 821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 GGCCAGTGAGCTGGGGAAGAGTACCAACACATTCTTCAAGCCCCCTTGTGTGAACGTGTT 128

Qy    822 ccgatgtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcgta 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 CCGATGTGGTGGCTGTTGCAATGAAGAGAGCCTTATCTGTATGAACACCAGCACCTCGTA 188

Qy    882 catttccaaacagctct 898
          ||||||||||||| | |
Db    189 CATTTCCAAACAGGTAT 205
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RESULT  14
HSY12867
LOCUS       HSY12867      169 bp    DNA             PRI       02-AUG-1999
DEFINITION  Homo sapiens FIGF gene, exon 4.
ACCESSION   Y12867
VERSION     Y12867.1  GI:2909355
KEYWORDS    FIGF gene; growth factor; VEGF-D.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 169)
  AUTHORS   Rocchigiani,M., Lestingi,M., Luddi,A., Orlandini,M., Franco,B.,
            Rossi,E., Ballabio,A., Zuffardi,O. and Oliviero,S.
  TITLE     Human FIGF: cloning, gene structure, and mapping to chromosome
            Xp22.1 between the PIGA and the GRPR genes
  JOURNAL   Genomics 47 (2), 207-216 (1998)
  MEDLINE   98140120
REFERENCE   2  (bases 1 to 169)
  AUTHORS   Oliviero,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) S. Oliviero, University of Siena,
            Department of Molecular Biology, Via Fiorentina 1, Siena, 53100,
            ITALY
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COMMENT     Related sequence: X99572.
FEATURES             Location/Qualifiers
     source          1. .169
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="p22.2"
                     /dev_stage="adult"
     gene            11. .159
                     /gene="FIGF"
     exon            11. .159
                     /gene="FIGF"
                     /number=4
                     /usedin=Y12864:FIGFCDS
                     /usedin=Y12864:FIGFmRNA
BASE COUNT       46 a     44 c     32 g     47 t
ORIGIN
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  Query Match             7.6%;  Score 151.4;  DB 10;  Length 169;
  Best Local Similarity   99.3%;  Pred. No. 3.6e-28;
  Matches  152;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     893 agctctttgagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttg 952
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 AGCTCTTTGAGATATCAGTGCCTTTGACATCAGTACCTGAATTAGTGCCTGTTAAAGTTG 68

Qy     953 ccaatcatacaggttgtaagtgcttgccaacagccccccgccatccatactcaattatca 1012
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 CCAATCATACAGGTTGTAAGTGCTTGCCAACAGCCCCCCCGCCATCCATACTCAATTATCA 128

Qy    1013 gaagatccatccagatccctgaagaagatcgct 1045
           |||||||||||||||||||||||||||||| |
Db     129 GAAGATCCATCCAGATCCCTGAAGAAGATCGGT 161
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RESULT  15
CCY15837
LOCUS       CCY15837     1257 bp    mRNA            VRT       06-MAY-1998
DEFINITION  Coturnix coturnix mRNA for vascular endothelial growth factor C.
ACCESSION   Y15837
VERSION     Y15837.1  GI:2687844
KEYWORDS    vascular endothelial growth factor C; VEGF-C gene.
SOURCE      quail.
  ORGANISM  Coturnix coturnix
            Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
            Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
REFERENCE   1  (bases 1 to 1257)
  AUTHORS   Eichmann,A., Corbel,C., Jaffredo,T., Breant,C., Joukov,V.,
            Kumar,V., Alitalo,K. and le Douarin,N.M.
  TITLE     Avian VEGF-C: cloning, embryonic expression pattern and stimulation
            of the differentiation of VEGFR2-expressing endothelial cell
            precursors
  JOURNAL   Development 125 (4), 743-752 (1998)
  MEDLINE   98167900
REFERENCE   2  (bases 1 to 1257)
  AUTHORS   Eichmann,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-1997) A. Eichmann, Institut d'Embryologie
            Cellulaire et Moleculaire du CNRS et du College de France, 49bis
            avenue de la Belle Gabrielle, 94736 Nogent sur Marne Cedex, FRANCE
FEATURES             Location/Qualifiers
     source          1. .1257
                     /organism="Coturnix coturnix"
                     /db_xref="taxon:9091"
                     /dev_stage="embryo"
                     /clone="1"
     sig_peptide     1. .93
                     /gene="VEGF-C"
     CDS             1. .1257
                     /gene="VEGF-C"
                     /codon_start=1
                     /product="vascular endothelial growth factor C"
                     /protein_id="CAA75799.1"
                     /db_xref="GI:2687845"
                     /db_xref="SPTREMBL:O57352"
                     /translation="MHLLEMLSLGCCLAAGAVLLGPRQPPVAAAYESGHGYYEEEPGA
                     GEPKAHASKDLEEQLRSVSSVDELMTVLYPEYWKMFKCQLRKGGWQHNREHSSSDTRS
                     DDSLKFAAAHYNAEILKSIDTEWRKTQCMPREVCVDVGKEFGATTNTFFKPPCVSIYR
                     CGGCCNSEGLQCMNISTNYISKTLFEITVPLSHGPKPVTVSFANHTSCRCMSKLDVYR
                     QVHSIIRRSLPATQTQCHVANKTCPKNHVWNNQICRCLAQHDFGFSSHLGDSDTSEGF
                     HICGPNKELDEETCQCVCKGGVRPISCGPHKELDRASCQCMCKNKLLPSSCGPNKEFD
                     EEKCQCVCKKTCPKHHPLNPAKCICECTESPNKCFLKGKRFHHQTCSCYRPPCTVRTK
                     RCDAGFLLAEEVCRCVRTSWKRPLMN"
     gene            1. .1257
                     /gene="VEGF-C"
     mat_peptide     331. .1254
                     /gene="VEGF-C"
                     /product="vascular endothelial growth factor C"
BASE COUNT      369 a    294 c    295 g    299 t
ORIGIN
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  Query Match             6.9%;  Score 138.8;  DB 4;  Length 1257;
  Best Local Similarity   52.8%;  Pred. No. 5.9e-25;
  Matches  380;  Conservative    0;  Mismatches  322;  Indels   18;  Gaps    3;

Qy     523 gaacagcagatcagggctgcttctagtttggaggaactacttcgaattactcactctgag 582
           ||| ||||| |  |  |||  || ||| |||| |||||  |   | |   | || | ||
Db     166 GAAGAGCAGTTGCGATCTGTGTCCAGTGTGGATGAACTCATGACAGTACTTTACCCAGAA 225

Qy     583 gactggaagctgtggagatgcaggctgaggctcaaaagttttaccagta---------- 632
           |||||||  |||  | |||   | |||||     | |||        |
Db     226 TACTGGAAAATGTTCAAATGTCAGTTGAGGAAAGGAGGTTGGCAACACAACAGGGAACAC 285

Qy     632 -tggactctcgctcagcatcccatcggtccactaggtttgcggcaactttctatgacatt 690
            ||||    ||  |||  ||   ||    |  ||||| ||| |    ||| |
Db     286 TCCAGCTCTGATACAAGATCAGATGATTCATTGAAATTTGCCGCAGCACATTATAATGCA 345

Qy     691 gaaacactaaaagttatagatgaagaatggcaaagaactcagtgcagccctagagaaacg 750
           || |  || |||  ||| |||   ||||||  || ||||||||||  ||  | ||| |
Db     346 GAGATCCTGAAAAGTATTGATACTGAATGGAGAAAAACTCAGTGCATGCCACGTGAAGTG 405

Qy     751 tgcgtggaggtggccagtgagctggggaagagtaccaacacattcttcaagccccccttgt 810
           || ||||| ||||  |  ||| | ||    | ||| ||||| ||||| || ||||| |||
Db     406 TGTGTGGATGTGGGGAAAGAGTTTGGAGCAACTACAAACACCTTCTTTAAACCCCCGTGT 465

Qy     811 gtgaacgtgttccgatgtggtggctgttgcaatgaagagagccttatctgtatgaacacc 870
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Db     466 GTATCCATCTACAGATGTGGAGGTTGCTGCAATAGTGAAGGACTCCAGTGTATGAATATC 525

Qy     871 agcacctcgtacatttccaaacagctctttgagatatcagtgcctttgacatcagtacct 930
           |||||    |||||  |||     | ||||||||  ||||||||  | |    |  ||
Db     526 AGCACAAATTACATCAGCAAGACATTGTTTGAGATTACAGTGCCTCTCTCTCATGGCCCC 585

Qy     931 gaattagtgcctgttaaagttgccaatcatacaggttgtaagtgcttgccaaca---gcc 987
           ||   ||  | || |   ||||||||| ||    ||    ||| || | |     |
Db     586 AAACCTGTAACAGTCAGTTTTGCCAATCACACGTCCTGCCGATGCATGTCTAAGTTGGAT 645

Qy     988 ccccgccatccatactcaattatcagaagatccatccagatccctgaagaagatcgctgt 1047
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Db     646 GTTTACAGACAAGTTCATTCTATCATAAGACGTTCCTTGCCAGCAACACAAACTCAGTGT 705

Qy    1048 tcccattccaagaaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgt 1107
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Db     706 CATGTGGCAAACAAGACCTGTCCAAAAAATCATGTCTGGAATAATCAGATTTGCAGATGC 765

Qy    1108 gttttgcaggaggaaaatccacttgctggaacagaagaccactctcatctccaggaacca 1167
           |    ||| | ||   |    |  ||          |   | ||| |       |||  |
Db     766 TTAGCACAGCACGATTTTGGTTTCTCTTCTCACCTTGGAGATTCTGACACATCTGAAGGA 825

Qy    1168 ---gctctctgtgggccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaaa 1224
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Db     826 TTCCATATTTGTGGGCCCAACAAAGAGCTGGATGAAGAAACCTGTCAATGCGTCTGCAAA 885
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Search completed: May 16, 2000, 14:35:16
Job time: 9110 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 16, 2000, 15:27:05 ; Search time 42.49 Seconds
(without alignments)
253.732 Million cell updates/sec

Title: US-09-214-982-1
Perfect score: 1963
Sequence: 1 MYREWVVVNVFMMLYVQLVQ.....HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	704.5	35.9	419	1	VEGC_HUMAN	P49767 homo sapien
2	696	35.5	415	1	VEGC_MOUSE	P97953 mus musculu
3	200	10.2	190	1	VEGF_BOVIN	P15691 bos taurus
4	198	10.1	190	1	VEGF_PIG	P49151 sus scrofa
5	198	10.1	214	1	VEGF_MOUSE	Q00731 mus musculu
6	196	10.0	215	1	VEGF_HUMAN	P15692 homo sapien
7	194	9.9	190	1	VEGF_RAT	P16612 rattus norv
8	185	9.4	164	1	VEGF_CAVPO	P26617 cavia porce
9	181.5	9.2	1700	1	BAR3_CHITE	Q03376 chironomus
10	176.5	9.0	188	1	VEGB_MOUSE	P49766 mus musculu
11	175.5	8.9	188	1	VEGB_HUMAN	P49765 homo sapien
12	167.5	8.5	146	1	VEGF_SHEEP	P50412 ovis aries
13	164	8.4	148	1	VEGH_ORFN7	P52585 orf virus (
14	161	8.2	245	1	PDGB_FELCA	P12919 felis silve
15	159.5	8.1	170	1	PLGF_HUMAN	P49763 homo sapien
16	155.5	7.9	216	1	VEGF_CHICK	P52582 gallus gall
17	155	7.9	158	1	PLGF_MOUSE	P49764 mus musculu
18	148	7.5	133	1	VEGH_ORFN2	P52584 orf virus (
19	145	7.4	241	1	PDGB_HUMAN	P01127 homo sapien
20	135	6.9	241	1	PDGB_MOUSE	P31240 mus musculu
21	134.5	6.9	241	1	PDGB_SHEEP	Q95229 ovis aries
22	133.5	6.8	225	1	PDGB_RAT	Q05028 rattus norv
23	125.5	6.4	211	1	PDGA_HUMAN	P04085 homo sapien
24	122	6.2	226	1	TSIS_SMSAV	P01128 simian sarc
25	120	6.1	226	1	PDGA_XENLA	P13698 xenopus lae
26	118	6.0	965	1	YNC3_YEAST	P53971 saccharomyc
27	115.5	5.9	1964	1	NTC4_MOUSE	P31695 mus musculu
28	113	5.8	204	1	PDGA_RAT	P28576 rattus norv
29	113	5.8	846	1	ITBX_DROME	P11584 drosophila
30	112	5.7	3635	1	LMA5_MOUSE	Q61001 mus musculu
31	111	5.7	213	1	PDGA_RABIT	P34007 oryctolagus
32	111	5.7	2201	1	TENA_HUMAN	P24821 homo sapien
33	109	5.6	677	1	SP87_DICDI	P54643 dictyosteli
34	109	5.6	1104	1	NFX1_HUMAN	Q12986 homo sapien
35	109	5.6	2871	1	FBN1_HUMAN	P35555 homo sapien
36	108	5.5	211	1	PDGA_MOUSE	P20033 mus musculu
37	108	5.5	1426	1	TOP_DROME	P04412 drosophila
38	108	5.5	4544	1	LRP1_HUMAN	Q07954 homo sapien
39	107.5	5.5	1178	1	TSP1_CHICK	P35440 gallus gall
40	107	5.5	1680	1	FUR2_DROME	P30432 drosophila
41	107	5.5	2907	1	FBN2_MOUSE	Q61555 mus musculu
42	106	5.4	1808	1	TENA_CHICK	P10039 gallus gall
43	105	5.3	1746	1	TENA_PIG	Q29116 sus scrofa
44	105	5.3	2911	1	FBN2_HUMAN	P35556 homo sapien
45	104	5.3	1038	1	SOG_DROME	Q24025 drosophila

ALIGNMENTS

RESULT 1
VEGC_HUMAN
ID VEGC_HUMAN STANDARD; PRT; 419 AA.
AC P49767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND).
GN VEGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RX MEDLINE; 96178224.
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RT "A novel vascular endothelial growth factor, VEGF-C, is a ligand for
RT the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
RL EMBO J. 15:290-298(1996).
RN [2]
RP ERRATUM.
RX MEDLINE; 96203094.
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RL EMBO J. 15:1751-1751(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96312526.
RA Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
RT "Vascular endothelial growth factor-related protein: a ligand and
RT specific activator of the tyrosine kinase receptor Flt4.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,
RA Burgess P., Giannotti J., Ciarletta A., Hennessey D., Kovacic S.,
RA Fitzgerald M., Scaltreto H., Weich N., Neben S., Finnerty H.,
RA Zollner R., Wang J., Nickbarg E., Gassaway R., Turner K.,
RA Wood C.R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- PTM: PROBABLY PROTEOLITICALLY PROCESSED IN THE C-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC ---

CC ---
DR EMBL; X94216; CAA63907.1; -.

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DR   EMBL; U43142; AAA85214.1; -.
DR   EMBL; U58111; AAB02909.1; -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 601528; -.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL        1      ?       POTENTIAL.
FT   PROPEP        ?    102       POTENTIAL.
FT   CHAIN       103    419       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN      275    365       4 X 24 AA TANDEM REPEATS.
FT   REPEAT      275    298       1.
FT   REPEAT      299    322       2.
FT   REPEAT      323    346       3.
FT   REPEAT      347    365       4 (PARTIAL).
FT   CARBOHYD    175    175       POTENTIAL.
FT   CARBOHYD    205    205       POTENTIAL.
FT   CARBOHYD    240    240       POTENTIAL.
SQ   SEQUENCE   419 AA;  46883 MW;  9F598719DB3E014F CRC64;


  Query Match             35.9%;  Score 704.5;  DB 1;  Length 419;
  Best Local Similarity   38.9%;  Pred. No. 1.3e-47;
  Matches  140;  Conservative   61;  Mismatches   88;  Indels   71;  Gaps   11;

Qy      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
           |:|:|: ||::||: : : | ||:::|:|| :   :::|| :  : :|||  |
Db      57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114

Qy      95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
           : | || || ||::||| ||| |::|  | | :||||||||||:|:|||||| | | ||
Db     115 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174

Qy     155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
           ||||||:|| ||||:|||:  |: | :  |||| |:|:      |  :||||||:  :|
Db     175 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 234

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE---------ENPLAGTED----HSHLQE--- 255
           :   |  : | || : :|::: |:|: ||         ::   |  |    :  | |
Db     235 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291

Qy     255 ---------PALCGPH----------------------MMFDEDRCECVCKTPCPKDL 281
                   || ||||                     |||: |:|||| ||::
Db     292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351

Qy     282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
             :|  |:| || || : |  | | ||  |||| : ||| : : ||    : :|
Db     352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC------YRRPCTNRQKACEPGFSYSEE 404


RESULT   2
VEGC_MOUSE
ID   VEGC_MOUSE     STANDARD;      PRT;   415 AA.
AC   P97953;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C).
GN   VEGFC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE; 97164697.
RA   Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M.,
RA   Joukov V., Alitalo K.;
RT   "VEGF-C receptor binding and pattern of expression with VEGFR-3
RT   suggests a role in lymphatic vascular development.";
RL   Development 122:3829-3837(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R., Burgess P.,
RA   Giannotti J., Ciarletta A., Hennessey D., Kovacic S., Fitzgerald M.,
RA   Scaltreto H., Weich N., Neben S., Finnerty H., Zollner R., Wang J.,
RA   Nickbarg E., Gassaway R., Turner K., Wood C.R.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U73620; AAC52984.1; -.
DR   EMBL; U58112; AAB46707.1; -.
DR   HSSP; P15692; 1VPF.
DR   MGD; MGI:109124; VEGFC.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL        1      ?       POTENTIAL.
FT   PROPEP        ?     98       POTENTIAL.
FT   CHAIN        99    415       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN      271    361       4 X 24 AA TANDEM REPEATS.
FT   REPEAT      271    294       1.
FT   REPEAT      295    318       2.
FT   REPEAT      319    342       3.
FT   REPEAT      343    361       4 (PARTIAL).
FT   CARBOHYD    171    171       POTENTIAL.
FT   CARBOHYD    201    201       POTENTIAL.
FT   CARBOHYD    236    236       POTENTIAL.
SQ   SEQUENCE   415 AA;  46471 MW;  D9D3DD3CECC659D6 CRC64;


  Query Match             35.5%;  Score 696;  DB 1;  Length 415;
  Best Local Similarity   38.6%;  Pred. No. 5.9e-47;
  Matches  140;  Conservative   57;  Mismatches   96;  Indels   70;  Gaps   11;

Qy      27 GPVKRSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRS 86
           | ||      |   |:|:|: ||:::||: : : : ||:::|:||   :      : :  |
Db      46 GEVKAFEGKDL---EEQLRSVSSVDELMSVLYPDYWKMYKCQLRKGGWQQPTLNTRTGDS 102

Qy      87 TRFAATFYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCC 146
            :|||  |: | || || ||::||| ||| |::|  | | :||||||||||:|:||||||
Db     103 VKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCC 162

Qy     147 NEESLICMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIR 204
           | | | |||||| |:|| ||||:|||:  |: | :  |||| |:|:      |  :||||
Db     163 NSEGLQCMNTSTGYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIR 222

Qy     205 RSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQ---------EENPLAGTED----H 249
           ||:   :|:   |  : | || : :|::  |:|: |         |::   |  |    :
Db     223 RSLPATLPQ---CQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVCGPN 279

Qy     250 SHLQE------------PALCGPH----------------------MMFDEDRCECVC 273
           | |             |: ||||                     |||: |:|||
Db     280 KELDEDTCQCVCKGGLRPSSCGPHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVC 339

Qy     274 KTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACA 333
           |  ||::   :|  |:| || |: : |  | | ||  ||||      : ||||:
Db     340 KRTCPRNQPLNPGKCAC-ECTENTQKCFLKGKKFHHQTCSC------YRRPCANR----L 388

Qy     334 KHC 336
           |||
Db     389 KHC 391
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```
RESULT   3
VEGF_BOVIN
ID   VEGF_BOVIN     STANDARD;      PRT;   190 AA.
AC   P15691;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX   MEDLINE; 90069608.
RA   Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT   "Vascular endothelial growth factor is a secreted angiogenic
RT   mitogen.";
RL   Science 246:1306-1309(1989).
RN   [2]
RP   SEQUENCE OF 27-190 FROM N.A.
RX   MEDLINE; 90121225.
RA   Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,
RA   Lau K., Crisp T., Fiddes J.C., Abraham J.A.;
RT   "Vascular endothelial growth factor: a new member of the platelet-
RT   derived growth factor gene family.";
RL   Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
RN   [3]
RP   SEQUENCE OF 27-31.
RX   MEDLINE; 89286596.
RA   Ferrara N., Henzel W.J.;
RT   "Pituitary follicular cells secrete a novel heparin-binding growth
RT   factor specific for vascular endothelial cells.";
RL   Biochem. Biophys. Res. Commun. 161:851-858(1989).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M32976; AAA30502.1; -.
DR   EMBL; M31836; AAA30804.1; -.
DR   EMBL; M33750; AAA30805.1; -.
DR   PIR; A33255; A33255.
DR   PIR; A33787; A33787.
DR   PIR; B40080; B40080.
DR   HSSP; P15692; 2VGH.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL       1     26
FT   CHAIN       27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID    51     93       BY SIMILARITY.
FT   DISULFID    82    127       BY SIMILARITY.
FT   DISULFID    86    129       BY SIMILARITY.
FT   DISULFID    76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   100    100       POTENTIAL.
FT   VARSPLIC    139    183       MISSING (IN ISOFORM BETA).
FT   VARSPLIC    184    184       R -> K (IN ISOFORM BETA).
SQ   SEQUENCE   190 AA;  22310 MW;  EDBF903E46E24789 CRC64;


  Query Match             10.2%;  Score 200;  DB 1;  Length 190;
  Best Local Similarity   25.4%;  Pred. No. 5.9e-09;
  Matches   57;  Conservative   21;  Mismatches   66;  Indels   80;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:||| |: |
Db      38 EVVKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
           |: |:  |                          |   :|         | |
Db      97 EEFNITMQIMRIK----------------------PHQSQH----------IGEMSFLQ 123

Qy     217 HSKKLCPIDMLWDSNKCKC-----VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC 271
           |             |||:|       ::|||               |||
Db     124 H------------NKCECRPKKDKARQENP---------------CGP----------- 145

Qy     272 VCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
            |         :| |: | |  || :   |  :    :  || |:
Db     145 -CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   4
VEGF_PIG
ID   VEGF_PIG       STANDARD;      PRT;   190 AA.
AC   P49151;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RX   MEDLINE; 95143284.
RA   Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
RT   "Nucleotide sequence and expression of the porcine vascular
RT   endothelial growth factor.";
RL   Biochim. Biophys. Acta 1260:235-238(1995).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X81380; CAA57143.1; -.
DR   HSSP; P15692; 2VGH.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL       1     26       POTENTIAL.
FT   CHAIN       27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID    51     93       BY SIMILARITY.
FT   DISULFID    82    127       BY SIMILARITY.
```

```
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       POTENTIAL.
SQ   SEQUENCE   190 AA;  22368 MW;  04D40B8D7913047F CRC64;


  Query Match             10.1%;  Score 198;  DB 1;  Length 190;
  Best Local Similarity   24.2%;  Pred. No. 8.4e-09;
  Matches   54;  Conservative   24;  Mismatches   67;  Indels   78;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : ||||||:| | |: |
Db      38 EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
             |: |:  |       |     :  :    |  |:|                    |::
Db      97 EEFNITMQIMRIK------PHQGQHIGEMSFLQHNKCECR----------------PKK 133

Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||                    ::|||              |||
Db     134 DRA--------------------RQENP--------------CGP------------ 145

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |        :| |: | |  || :   |  :    :  || |:
Db     145 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   5
VEGF_MOUSE
ID   VEGF_MOUSE     STANDARD;      PRT;   214 AA.
AC   Q00731;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92274860.
RA   Breier G., Albrecht U., Sterrer S., Risau W.;
RT   "Expression of vascular endothelial growth factor during embryonic
RT   angiogenesis and endothelial cell differentiation.";
RL   Development 114:521-532(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (VEGF-1).
RX   MEDLINE; 92355593.
RA   Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT   "Vascular endothelial growth factor. Regulation by cell
RT   differentiation and activated second messenger pathways.";
RL   J. Biol. Chem. 267:16317-16322(1992).
RN   [3]
RP   SEQUENCE OF 1-3 FROM N.A.
RX   MEDLINE; 96216498.
RA   Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore P.A.;
RT   "The mouse gene for vascular endothelial growth factor. Genomic
RT   structure, definition of the transcriptional unit, and
RT   characterization of transcriptional and post-transcriptional
RT   regulatory sequences.";
RL   J. Biol. Chem. 271:3877-3883(1996).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: VEGF-1 AND VEGF-2 ARE SECRETED WHILE
CC       VEGF-3 REMAINS CELL-SURFACE ASSOCIATED UNLESS RELEASED BY
CC       HEPARIN.
CC   -!- ALTERNATIVE PRODUCTS: THREE FORMS (VEGF-1, VEGF-2 AND VEGF-3) ARE
CC       PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. THE
CC       LONGEST FORM (VEGF-3, SHOWN HERE) CONTAINS A BASIC INSERT LINKED
CC       TO CELL-ASSOCIATION/HEPARIN-BINDING.
CC   -!- TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED MAINLY IN
CC       THE CHOROID PLEXUS, PARAVENTRICULAR NEUROEPITHELIUM, PLACENTA AND
CC       KIDNEY GLOMERULI. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADRENAL
CC       GLAND AND IN SEMINIFEROUS TUBULES OF TESTIS. HIGH EXPRESSION OF
CC       VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S37052; AAB22252.1; -.
DR   EMBL; S38083; AAB22253.1; -.
DR   EMBL; S38100; AAB22254.1; -.
DR   EMBL; M95200; AAA40547.1; -.
DR   EMBL; U41383; CAB35545.1; -.
DR   PIR; A43351; A43351.
DR   HSSP; P15692; 2VGH.
DR   MGD; MGI:103178; VEGF.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    214       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       PROBABLE.
FT   VARSPLIC    140    140       K -> N (IN ISOFORM VEGF-1).
FT   VARSPLIC    141    164       MISSING (IN ISOFORM VEGF-1).
FT   VARSPLIC    141    208       MISSING (IN ISOFORM VEGF-2).
FT   CONFLICT    117    118       GE -> ER (IN REF. 2).
SQ   SEQUENCE   214 AA;  25283 MW;  B5540B51E4BB6E17 CRC64;


  Query Match             10.1%;  Score 198;  DB 1;  Length 214;
  Best Local Similarity   23.7%;  Pred. No. 9.5e-09;
  Matches   63;  Conservative   35;  Mismatches   94;  Indels   74;  Gaps   11;

Qy      62 WKLWRCRLRL--------KSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113
           |  |   | |          ::  : :    ||           | :| :|  :||: | |
Db       7 WVHWTLALLLYLHHAKWSQAAPTTEGEQKSH-----------EVIKFMD-VYQRSYCRP 53

Qy     114 RETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLT 173
            || |::  |        ||| || : || ||||:|:| |: || | |: |:  |  |
Db      54 IETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPTSESNITMQIMRIK-PHQ 112

Qy     174 SVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKC 233
           |   :  :    |: |:|                  |::||    ||      :    |
Db     113 S-QHIGEMSFLQHSRCECR----------------PKKDRTKPEKK-----SVRGKGKG 149

Qy     234 KCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKD----LIQHPKNCS 289
           :  ::::     |                      ||     || :      :| |: |
Db     150 QKRKRKKSRFKSWSVH----------------CE-----PCSERRKHLFVQDPQTCK 185

Qy     290 CFECKESLETCCQKHKLFHPDTCSCE 315
           |  || :   |  :    :  || |:
Db     186 C-SCKNTDSRCKARQLELNERTCRCD 210


RESULT   6
VEGF_HUMAN
ID   VEGF_HUMAN     STANDARD;      PRT;   215 AA.
AC   P15692;
DT   01-APR-1990 (Rel. 14, Created)
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DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF OR VEGFA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90069608.
RA   Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT   "Vascular endothelial growth factor is a secreted angiogenic
RT   mitogen.";
RL   Science 246:1306-1309(1989).
RN   [2]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE; 90069609.
RA   Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
RA   Connolly D.T.;
RT   "Vascular permeability factor, an endothelial cell mitogen related to
RT   PDGF.";
RL   Science 246:1309-1312(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91268072.
RA   Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
RA   Fiddes J.C., Abraham J.A.;
RT   "The human gene for vascular endothelial growth factor. Multiple
RT   protein forms are encoded through alternative exon splicing.";
RL   J. Biol. Chem. 266:11947-11954(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92231879.
RA   Weindel K., Marme D., Weich H.A.;
RT   "AIDS-associated Kaposi's sarcoma cells in culture express vascular
RT   endothelial growth factor.";
RL   Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
RN   [5]
RP   PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX   MEDLINE; 90062112.
RA   Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA   Siegel N., Haymore B.L., Leimgruber R., Feder J.;
RT   "Human vascular permeability factor. Isolation from U937 cells.";
RL   J. Biol. Chem. 264:20017-20024(1989).
RN   [6]
RP   SEQUENCE OF 27-41.
RX   MEDLINE; 93145946.
RA   Fiebich B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,
RA   Kochs G., Marme D., Hug H., Weich H.A.;
RT   "Synthesis and assembly of functionally active human vascular
RT   endothelial growth factor homodimers in insect cells.";
RL   Eur. J. Biochem. 211:19-26(1993).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX   MEDLINE; 97352774.
RA   Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA   de Vos A.M.;
RT   "Vascular endothelial growth factor: crystal structure and functional
RT   mapping of the kinase domain receptor binding site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX   MEDLINE; 98035455.
RA   Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT   "The crystal structure of vascular endothelial growth factor (VEGF)
RT   refined to 1.93-A resolution: multiple copy flexibility and receptor
RT   binding.";
RL   Structure 5:1325-1338(1997).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX   MEDLINE; 99119204.
RA   Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA   Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT   "Crystal structure of the complex between VEGF and a receptor-blocking
RT   peptide.";
RL   Biochemistry 37:17765-17772(1998).
RN   [10]
RP   STRUCTURE BY NMR OF 34-135.
RX   MEDLINE; 97477915.
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "1H, 13C, and 15N backbone assignment and secondary structure of the
RT   receptor-binding domain of vascular endothelial growth factor.";
RL   Protein Sci. 6:2250-2260(1997).
RN   [11]
RP   STRUCTURE BY NMR OF 137-215.
RX   MEDLINE; 98298440.
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "Solution structure of the heparin-binding domain of vascular
RT   endothelial growth factor.";
RL   Structure 6:637-648(1998).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: FOUR FORMS OF VEGF ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE (VEGF-121, VEGF-165,
CC       VEGF-189 AND VEGF-215).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M32977; AAA35789.1; -.
DR   EMBL; M27281; AAA36807.1; -.
DR   EMBL; M63978; AAA36804.1; -.
DR   EMBL; M63971; AAA36804.1; JOINED.
DR   EMBL; M63972; AAA36804.1; JOINED.
DR   EMBL; M63973; AAA36804.1; JOINED.
DR   EMBL; M63974; AAA36804.1; JOINED.
DR   EMBL; M63975; AAA36804.1; JOINED.
DR   EMBL; M63976; AAA36804.1; JOINED.
DR   EMBL; M63977; AAA36804.1; JOINED.
DR   EMBL; X62568; CAA44447.1; -.
DR   PIR; A34492; A34492.
DR   PIR; A40079; A40079.
DR   PIR; A40080; A40080.
DR   PIR; A40454; A40454.
DR   PIR; B40454; B40454.
DR   PIR; C40454; C40454.
DR   PIR; JQ1463; JQ1463.
DR   PIR; JQ1464; JQ1464.
DR   PIR; S17348; S17348.
DR   PDB; 1VGH; 08-APR-98.
DR   PDB; 2VGH; 08-APR-98.
DR   PDB; 1VPF; 08-APR-98.
DR   PDB; 2VPF; 29-JUL-98.
DR   PDB; 1VPP; 23-FEB-99.
DR   MIM; 192240; -.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal;
KW   3D-structure.
FT   SIGNAL       1     26
FT   CHAIN       27    215       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     52     94
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FT   DISULFID     83    128
FT   DISULFID     87    130
FT   DISULFID     77     77       INTERCHAIN.
FT   DISULFID     86     86       INTERCHAIN.
FT   CARBOHYD    101    101
FT   VARSPLIC    141    141       K -> N (IN ISOFORM VEGF-121 AND ISOFORM
FT                                VEGF-165).
FT   VARSPLIC    142    165       MISSING (IN ISOFORM VEGF-165).
FT   VARSPLIC    142    209       MISSING (IN ISOFORM VEGF-121).
SQ   SEQUENCE   215 AA;  25173 MW;  7B9759AD5871FF33 CRC64;


  Query Match             10.0%;  Score 196;  DB 1;  Length 215;
  Best Local Similarity   25.6%;  Pred. No. 1.4e-08;
  Matches   57;  Conservative   26;  Mismatches   86;  Indels   54;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |       ||| || : ||||||:| | |: |
Db      39 EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 97

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
             | |: |:  |       |     :  :    |  |:|                  |::
Db      98 EESNITMQIMRIK------PHQGQHIGEMSFLQHNKCECR----------------PKK 134

Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||    ||        | : |   |:       :   :      |||
Db     135 DRARQEKK---------SVRGKGKGQKRK----RKKSRYKSWSVPCGP------------ 170

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |       :| |: | |  || :   |  :    :  || |:
Db     170 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 211


RESULT   7
VEGF_RAT
ID   VEGF_RAT       STANDARD;      PRT;   190 AA.
AC   P16612;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-190.
RX   MEDLINE; 90207249.
RA   Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
RA   Palisi T.M., Hope D.A., Thomas K.A.;
RT   "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
RT   that is homologous to platelet-derived growth factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE PITUITARY, IN BRAIN, IN
CC       PARTICULARLY IN SUPRAOPTIC AND PARAVENTRICULAR NUCLEI AND THE
CC       CHOROID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTEUM OF
CC       THE OVARY AND IN KIDNEY GLOMERULI.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M32167; AAA41211.1; -.
DR   PIR; A35987; A35987.
DR   HSSP; P15692; 2VGH.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100
SQ   SEQUENCE   190 AA;  22396 MW;  589374010441F377 CRC64;


  Query Match             9.9%;  Score 194;  DB 1;  Length 190;
  Best Local Similarity   23.8%;  Pred. No. 1.7e-08;
  Matches   53;  Conservative   27;  Mismatches   65;  Indels   78;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |       ||| || : || ||||:|:| |: |
Db      38 EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPT 96

Qy     157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
           | | :: |:  |  |  |   :  :    |: |:|                  |::||
Db      97 SESNVTMQIMRIK-PHQS-QHIGEMSFLQHSRCECR----------------PKKDRTK 137

Qy     217 HSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTP 276
                                                          |: ||     |
Db     138 ----------------------------------------------PENHCE-----P 144

Qy     277 CPKD----LIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |  :     :| |: | |  || :   |  :    :  || |:
Db     145 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   8
VEGF_CAVPO
ID   VEGF_CAVPO     STANDARD;      PRT;   164 AA.
AC   P26617;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY
DE   FACTOR) (VPF).
GN   VEGF.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Berse B.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
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CC   ----------------------------------------------------------------------
DR   EMBL; M84230; AAA37057.1; -.
DR   HSSP; P15692; 2VGH.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein.
FT   DISULFID     25     67       BY SIMILARITY.
FT   DISULFID     56    101       BY SIMILARITY.
FT   DISULFID     60    103       BY SIMILARITY.
FT   DISULFID     50     50       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     59     59       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     74     74       POTENTIAL.
SQ   SEQUENCE   164 AA;  19330 MW;  9EB86A81A9D5DCA4 CRC64;


  Query Match             9.4%;  Score 185;  DB 1;  Length 164;
  Best Local Similarity   24.1%;  Pred. No. 7.3e-08;
  Matches   54;  Conservative   23;  Mismatches   67;  Indels   80;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  ::|: | | |  |::  |        ||| || : ||||||:||| |: |
Db      12 EEVKFMD-VYKRSYCRPIEMLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDESLECVPT 70

Qy     157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
               |: |:  |                         |   :|          | |
Db      71 EEFNITMQIMRIK----------------------PHQGQH----------IGEMSFLQ 97

Qy     217 HSKKLCPIDMLWDSNKCKC-----VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC 271
           ||             ||:|       ::|||               |||
Db      98 HS-------------KCECRPKKEKARQENP--------------CGP----------- 119

Qy     272 VCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
            |          :| |: | |  |: :   |  :   :  || |:
Db     119 -CSERRKHLFVQDPQTCKC-SCRNTDSRCKARQLELNERTCRCD 160


RESULT   9
BAR3_CHITE
ID   BAR3_CHITE     STANDARD;      PRT;  1700 AA.
AC   Q03376;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   01-OCT-1994 (Rel. 30, Last annotation update)
DE   BALBIANI RING PROTEIN 3 PRECURSOR.
GN   BR3.
OS   Chironomus tentans (Midge).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC   Chironomoidea; Chironomidae; Chironominae; Chironomus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RX   MEDLINE; 90172404.
RA   Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;
RT   "The Balbiani ring 3 gene in Chironomus tentans has a diverged
RT   repetitive structure split by many introns.";
RL   J. Mol. Biol. 211:331-349(1990).
CC   -!- FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR
CC       STRUCTURE, THE LARVAL TUBE. BALBIANI RING PROTEIN 3 COULD PLAY A
CC       ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS
CC       INTRACELLULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THESE
CC       FROM FORMING WATER-INSOLUBLE FIBERS TOO EARLY.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: SALIVARY GLAND.
CC   -!- DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X52263; CAA36506.1; -.
DR   PIR; S08167; S08167.
DR   HSSP; P18055; 2MRB.
DR   PRINTS; PR00876; MTNEMATODE.
KW   Repeat; Signal.
FT   SIGNAL       1      ?       POTENTIAL.
FT   CHAIN        ?   1700       BALBIANI RING PROTEIN 3.
SQ   SEQUENCE   1700 AA;  186145 MW;  34202B28521B0815 CRC64;


  Query Match             9.2%;  Score 181.5;  DB 1;  Length 1700;
  Best Local Similarity   19.9%;  Pred. No. 1.5e-06;
  Matches   68;  Conservative   43;  Mismatches  105;  Indels  125;  Gaps   15;

Qy     109 TQCSPRETCVEVASELGKSTNTFFKPPCVNVFR-----CGGCCNEESLICMNTSTSYISK 163
           |:|| ::  :|   | |  | |     | : ||     ||  |:::   |         |
Db    1073 TKCSDKQKFIESKCECGCETQT----QCKDGFRWSNLECGCLCDDKK--CP-------GK 1119

Qy     164 QLFEISVPLTSVPELVPVKVANH--------TGCKCLPTAPRHPYSIIRR------SIQI 209
           |:|: :     |   |     :          |||    | :  : ::          :
Db    1120 QVFDKNTCQCKCPNQKPGDTCGNGKDFCPLDCSCKCKNPKPANGCTGVQEWNEEKCQCEC 1179

Qy     210 PEE-------------------------DRCSHSKKL-----------------CPIDML 227
           |::                          ||:::|                    || : :
Db    1180 PKDKPKKQCPGGQDWNNHQCQCGCPTPAPTCSNNQKYSNVSCSCGCNPGKPKNGCPGNQI 1239

Qy     228 WDSNKCKCVLQE--ENP-----------------------------------LAGTEDH 249
           |  | |:||  :  | |                                       |
Db    1240 WCDNTCRCVCPKNMEKPADNCKTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECP 1299

Qy     250 SHLQEPALCGPHMMFDEDRCECVCKTP-----CPKDLIQHPKNCSCFECKESLETCCQKH 304
           :   :|| ||    :::| | | ||:      || :   : |:|   ||| |    |
Db    1300 ADKAKPASCGDKKSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDC---ECKCSATGNCPAG 1356

Qy     305 KLFHPDTCSCEDRCPFHTRPCASGKTACAKHCR--FPKEKR 343
           : ::  || |   ||  |  |   :  |:| |:   | :|:
Db    1357 QTWNSQTCQCS--CP-ATGKCTGAQVWCSKACKCVCPAQKK 1394


RESULT  10
VEGB_MOUSE
ID   VEGB_MOUSE     STANDARD;      PRT;   188 AA.
AC   P49766;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
DE   ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
GN   VEGFB OR VRF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RX   MEDLINE; 96197355.
RA   Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA   Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson U.;
RT   "Vascular endothelial growth factor B, a novel growth factor for
RT   endothelial cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 96183052.
RA   Townson S., Lagercrantz J., Grimmond S., Silins G.,
RA   Nordenskjold M., Weber G., Hayward N.K.;
RT   "Characterization of the murine VEGF-related factor gene.";
RL   Biochem. Biophys. Res. Commun. 220:922-928(1996).
CC   -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC       WITH VEGF.
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CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
CC       AND SKELETAL MUSCLE.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U48800; AAB06273.1; -.
DR   EMBL; U43837; AAC52553.1; -.
DR   HSSP; P15692; 2VGH.
DR   MGD; MGI:106199; VEGFB.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Signal; Heparin-binding.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    188       VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ   SEQUENCE   188 AA;  21442 MW;  D52A055FB995E9CA CRC64;


  Query Match             9.0%;  Score 176.5;  DB 1;  Length 188;
  Best Local Similarity   23.3%;  Pred. No. 3.8e-07;
  Matches   49;  Conservative   22;  Mismatches   70;  Indels   69;  Gaps    7;

Qy     106 WQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQL 165
           : |  | |||  | :: ||  :      | || | |||||| :: | |: |    :  |:
Db      42 YARATCQPREVVVPLSMELMGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQI 101

Qy     166 FEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPID 225
           |  | : : |:    :  |: |:| |          : |   |:  |      |||
Db     102 LMIQYPSSQLGEM---SLEEHSQCECRPKK--------KESAVKPDSPRI-----LCP-- 144

Qy     226 MLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHP 285
                 | : : |                                             |
Db     144 --------PCTQRRQRP-----------------------------------------DP 154

Qy     286 KNCSCFECKESLETCCQKHKL-FHPDTCSC 314
           : | |  |:      ||   |  :|||| |
Db     155 RTCRC-RCRRRRFLHCQGRGLELNPDTCRC 183


RESULT  11
VEGB_HUMAN
ID   VEGB_HUMAN     STANDARD;      PRT;   188 AA.
AC   P49765;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
DE   FACTOR).
GN   VEGFB OR VRF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96197355.
RA   Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA   Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson U.;
RT   "Vascular endothelial growth factor B, a novel growth factor for
RT   endothelial cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97077124.
RA   Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S.,
RA   Pollock P., Gotley D., Carson E., Rakar S., Nordenskjold M., Ward L.,
RA   Hayward N., Weber G.;
RT   "Cloning and characterization of a novel human gene related to
RT   vascular endothelial growth factor.";
RL   Genome Res. 6:124-131(1996).
CC   -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC       WITH VEGF.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC       HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U48801; AAB06274.1; -.
DR   EMBL; U43369; AAA91463.1; -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 601398; -.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Signal; Heparin-binding.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    188       VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ   SEQUENCE   188 AA;  21261 MW;  F04654D5A3727194 CRC64;


  Query Match             8.9%;  Score 175.5;  DB 1;  Length 188;
  Best Local Similarity   24.0%;  Pred. No. 4.6e-07;
  Matches   52;  Conservative   23;  Mismatches   73;  Indels   69;  Gaps    8;

Qy     100 KVID--EEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTS 157
           ||:   : : |  | |||  | :  ||  :      | || | |||||| :: | |: |
Db      34 KVVSWIDVYTRATCQPREVVVPLTVELMGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTG 93

Qy     158 TSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSH 217
           :  |:  |  | : : |:    :  |: |:| |          : |   |:  |
Db      94 QHQVRMQILMIRYPSSQLGEM---SLEEHSQCECRPKK--------KDSAVKPDSPR--- 140

Qy     218 SKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPC 277
           |||        :|           | | |      |   | | |:
Db     140 --PLCP----------RCT-------------QHHQRP---------DPRTCRCRCR--- 163

Qy     278 PKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSC 314
                       : |   |  :    :|||| |
Db     163 ---------------RRSFLRCQGRGLELNPDTCRC 183


RESULT  12
VEGF_SHEEP
ID   VEGF_SHEEP     STANDARD;      PRT;   146 AA.
AC   P50412;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Caprinae; Ovis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 97117958.
RA   Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
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RA   Reynolds L.P., Moor R.M.;
RT   "Characterization and expression of vascular endothelial growth
RT   factor (VEGF) in the ovine corpus luteum.";
RL   J. Reprod. Fertil. 108:157-165(1996).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X89506; CAA61677.1; -.
DR   HSSP; P15692; 1VPF.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL       1     26       BY SIMILARITY.
FT   CHAIN       27    146       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID    51     93       BY SIMILARITY.
FT   DISULFID    82    127       BY SIMILARITY.
FT   DISULFID    86    129       BY SIMILARITY.
FT   DISULFID    76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   100    100       POTENTIAL.
SQ   SEQUENCE   146 AA;  17247 MW;  4E792CB557F91760 CRC64;


  Query Match             8.5%;  Score 167.5;  DB 1;  Length 146;
  Best Local Similarity   38.1%;  Pred. No. 1.5e-06;
  Matches   37;  Conservative   14;  Mismatches   43;  Indels    3;  Gaps    3;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:||| |: |
Db      38 EVMKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLP 193
               |: |:  |  |  |   :  :    |  |:| |
Db      97 EEFNITMQIMRIK-PHQS-QHIGEMSFLQHNKCECRP 131


RESULT  13
VEGH_ORFN7
ID   VEGH_ORFN7     STANDARD;      PRT;   148 AA.
AC   P52585;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.
GN   A2R.
OS   Orf virus (strain NZ7) (OV NZ-7).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94076465.
RA   Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;
RT   "Homologs of vascular endothelial growth factor are encoded by the
RT   poxvirus orf virus.";
RL   J. Virol. 68:84-92(1994).
CC   -!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S67522; AAB29223.1; -.
DR   HSSP; P15692; 1VPF.
DR   PROSITE; PS00249; PDGF; FALSE_NEG.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL       1      ?       POTENTIAL.
FT   CHAIN        ?    148       VASCULAR ENDOTHELIAL GROWTH FACTOR
FT                               HOMOLOG.
FT   DISULFID    46     88       BY SIMILARITY.
FT   DISULFID    77    130       BY SIMILARITY.
FT   DISULFID    81    132       BY SIMILARITY.
FT   DISULFID    71     71       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    80     80       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    95     95       POTENTIAL.
SQ   SEQUENCE   148 AA;  16078 MW;  F0E13BA104CC73F8 CRC64;


  Query Match             8.4%;  Score 164;  DB 1;  Length 148;
  Best Local Similarity   32.8%;  Pred. No. 2.8e-06;
  Matches   38;  Conservative   12;  Mismatches   40;  Indels   26;  Gaps    4;

Qy     105 EWQRT----QCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSY 160
           :| ||     | ||:| | :  |  :|||  : | || | || |||| :  ||    |
Db      36 DWMRTLDKSGCKPRDTVVYLGEEYPESTNLQYNPRCVTVKRCSGCCNGDGQICTAVETRN 95

Qy     161 ISKQLFEISVPLTSV-----------PELVPVKVANHTGCKCL------PTAPRHP 199
           :     ::| :| |              |  : |  || | |:      ||  | |
Db      96 TT-----VTVSVTGVSSSSGTNSGVSTNLQRISVTEHTKCDCIGRTTTPTTTREP 146


RESULT  14
PDGB_FELCA
ID   PDGB_FELCA     STANDARD;      PRT;   245 AA.
AC   P12919;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
DE   (PDGFB) (PDGF-2).
GN   PDGFB OR C-SIS.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87146463.
RA   van den Ouweland A.M.W., van Groningen J.J.M., Schalken J.A.,
RA   van Neck H.W., Bloemers H.P.J., van de Ven W.J.M.;
RT   "Genetic organization of the c-sis transcription unit.";
RL   Nucleic Acids Res. 15:959-970(1987).
RN   [2]
RP   REVISIONS.
RA   van den Ouweland A.M.W.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC       CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC       AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC       RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC       IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC   -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC       AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC       TRANSFORMATION PROCESSES.
CC   -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC       PDGF RECEPTOR.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X05112; CAA28758.1; ALT_SEQ.
DR   PIR; A26402; TVCTSS.
DR   HSSP; P01127; 1PDG.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Proto-oncogene; Platelet; Signal.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   PROPEP       21     81
FT   CHAIN        82    194       PLATELET-DERIVED GROWTH FACTOR, B CHAIN.
FT   PROPEP      195    245
FT   DISULFID    101    145       BY SIMILARITY.
FT   DISULFID    134    182       BY SIMILARITY.
FT   DISULFID    138    184       BY SIMILARITY.
FT   DISULFID    128    128       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    137    137       INTERCHAIN (BY SIMILARITY).
SQ   SEQUENCE   245 AA;  27787 MW;  E7715291D9837512 CRC64;


  Query Match             8.2%;  Score 161;  DB 1;  Length 245;
  Best Local Similarity   29.9%;  Pred. No. 7.9e-06;
  Matches   67;  Conservative   24;  Mismatches  103;  Indels   30;  Gaps   10;

Qy       1 MYREWVVVNVFMML--YVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITH 58
           | | |    :|: |  |::||   | |  |:       |  |:  ||   | ::| |: |
Db       1 MNRCWA---LFLSLCCYLRLV---SAEGDPIPEELYKML--SDHSIR---SFDDLQRLLH 49

Qy      59 SEDWKLWRCRLRLKSFTS-----MDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113
             :     |  | | |  |     ::| |   ||   ||    :   :| |      |
Db      50 GDSVDEDRAELDLNSTRSHCGGELESLSRGRRSLGEAAGSPTVAEPAMIAE------CKT 103

Qy     114 RETCVEVASELGKSTNTFFK--PPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEIS-V 170
           |    ||:  |   ||  |   |||| | || ||||  :: |  |       |: :|  |
Db     104 RTEVFEVSRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRLVQVRKIEIV 163

Qy     171 PLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDR 214
             | :   | : :|  |||      |   : ||   :| |
Db     164 RKRPVFKKATVTLEDHLACKCETVVAARP---VTRSPGSSQEQR 204


RESULT  15
PLGF_HUMAN
ID   PLGF_HUMAN     STANDARD;      PRT;   170 AA.
AC   P49763;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   PLACENTA GROWTH FACTOR PRECURSOR (PLGF-1/PLGF-2).
GN   PGF OR PLGF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A. (PLGF-1).
RC   TISSUE=PLACENTA;
RX   MEDLINE; 92021031.
RA   Maglione D., Guerriero G., Viglietto G., Delli-Bovi P., Persico M.G.;
RT   "Isolation of a human placenta cDNA coding for a protein related to
RT   the vascular permeability factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:9267-9271(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (PLGF-2).
RC   TISSUE=PLACENTA;
RX   MEDLINE; 94198032.
RA   Hauser S., Weich H.A.;
RT   "A heparin-binding form of placenta growth factor (PlGF-2) is
RT   expressed in human umbilical vein endothelial cells and in
RT   placenta.";
RL   Growth Factors 9:259-268(1993).
RN   [3]
RP   SEQUENCE FROM N.A. (PLGF-2).
RX   MEDLINE; 93205407.
RA   Maglione D., Guerriero V., Viglietto G., Ferraro M.G., Aprelikova O.,
RA   Alitalo K., del Vecchio S., Lei K.-J., Chou J.Y., Persico M.G.;
RT   "Two alternative mRNAs coding for the angiogenic factor, placenta
RT   growth factor (PlGF), are transcribed from a single gene of
RT   chromosome 14.";
RL   Oncogene 8:925-931(1993).
RN   [4]
RP   CHARACTERIZATION, AND SEQUENCE OF 19-24.
RX   MEDLINE; 95014370.
RA   Park J.E., Chen H.H., Winer J., Houck K.A., Ferrara N.;
RT   "Placenta growth factor. Potentiation of vascular endothelial growth
RT   factor bioactivity, in vitro and in vivo, and high affinity binding
RT   to Flt-1 but not to Flk-1/KDR.";
RL   J. Biol. Chem. 269:25646-25654(1994).
CC   -!- FUNCTION: GROWTH FACTOR OF UNKNOWN FUNCTION. IT BINDS TO FMS-LIKE
CC       TYROSINE KINASE (FLT-1) AND THE LONGER FORM (PLGF-2) CAN ALSO
CC       BIND HEPARIN. IT IS ABLE TO POTENTIATE THE ACTION OF LOW LEVELS OF
CC       VEGF.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: BOTH FORMS ARE SECRETED BUT THE LONGER FORM
CC       APPEARS TO REMAIN CELL ATTACHED UNLESS RELEASED BY HEPARIN.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS; PLGF-1 AND PLGF-2 (SHOWN HERE);
CC       ARE PRODUCED BY ALTERNATIVE SPLICING. PLGF-1 DIFFERS FROM PLGF-2
CC       IN LACKING A 21 RESIDUES SEGMENT IN THE C-TERMINAL SECTION WHICH
CC       ACTS AS A CELL RETENTION SIGNAL.
CC   -!- TISSUE SPECIFICITY: WHILE BOTH FORMS ARE PRESENT IN MOST PLACENTAL
CC       TISSUES, THE LONGER FORM IS SPECIFIC TO EARLY (8 WEEK) PLACENTA
CC       AND ONLY THE SHORTER FORM IS FOUND IN THE COLON AND MAMMARY
CC       CARCINOMAS.
CC   -!- PTM: N-GLYCOSYLATED.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X54936; CAA38698.1; -.
DR   EMBL; A18411; CAA01393.1; -.
DR   EMBL; S72960; AAB30462.1; -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 601121; -.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Alternative splicing;
KW   Heparin-binding.
FT   SIGNAL        1     18
FT   CHAIN        19    170       PLACENTA GROWTH FACTOR.
FT   DISULFID     52     94       BY SIMILARITY.
FT   DISULFID     83    128       BY SIMILARITY.
FT   DISULFID     87    130       BY SIMILARITY.
FT   DISULFID     77     77       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     86     86       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     33     33       POTENTIAL.
FT   CARBOHYD    101    101       POTENTIAL.
FT   VARSPLIC    142    162       MISSING (IN ISOFORM PLGF-1).
FT   CONFLICT     91     91       D -> N (IN REF. 2).
SQ   SEQUENCE   170 AA;  19325 MW;  E47639AC59C0963F CRC64;


  Query Match             8.1%;  Score 159.5;  DB 1;  Length 170;
  Best Local Similarity   28.3%;  Pred. No. 7.1e-06;
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  Matches   39;  Conservative   25;  Mismatches   57;  Indels   17;  Gaps    4;

Qy      63 KLWRCRLRLKSFTSMD-------SRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           :|: | |:| :  ::        : || : |:       ::| :    | | |: |   |
Db       5 RLFPCFLQLLAGLALPAVPPQQWALSAGNGSS-------EVEVVP-FQEVWGRSYCRALE 56

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
             |:| ||         | | ||:: || ||| :| | |:   |: :: || :|
Db      57 RLVDVVSEYPSEVEHMFSPSCVSLLRCTGCCGDEDLHCVPVETANVTMQLLKIR--SGDR 114

Qy     176 PELVPVKVANHTGCKCLP 193
           |  | :  : |  |:| |
Db     115 PSYVELTFSQHVRCECRP 132


Search completed: May 16, 2000, 16:43:00
Job time: 4555 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 16, 2000, 12:04:38 ; Search time 69.55 Seconds
(without alignments)
7208.985 Million cell updates/sec

Title: US-09-214-982-2
Perfect score: 2004
Sequence: 1 ccagctttctgtarctgtaa.....aaacaccattattcaagtct 2004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2002.8	99.9	2004	1	V15156	Human vascular end
2	1998.6	99.7	2029	1	V20807	Homo sapiens vascu
3	1817.8	90.7	1864	1	T62961	Human c-Fos induce
4	1070.8	53.4	2846	1	V20806	Homo sapiens vascu
5	1065.6	53.2	1107	1	V32823	Human zvegf2 growt
6	977	48.8	1890	1	T62960	Murine c-Fos induc
7	877.2	43.8	1581	1	V15177	Mouse vascular end
8	874.8	43.7	1325	1	V20808	Mus musculus vascu
9	806.6	40.2	1491	1	V15178	Rat vascular endot
10	796.4	39.7	1135	1	V20809	Mus musculus vascu
11	137.6	6.9	1836	1	T84277	Mouse Flt4 recepto
12	137.6	6.9	1836	1	V52577	Mouse vascular end
13	134	6.7	1741	1	T84300	Quail Flt4 recepto
14	134	6.7	1741	1	V52578	Quail vascular end
15	129	6.4	1674	1	T51371	Human vascular end
16	129	6.4	1997	1	T84276	Human Flt4 recepto
17	129	6.4	1997	1	V52576	Human vascular end
18	129	6.4	2031	1	T59929	Human vascular end
19	129	6.4	2321	1	T68811	Human foetal liver
20	125.8	6.3	1525	1	T03950	DNA encoding vascu
21	64	3.2	299	1	T59930	EST HSC1WF111. Hum
22	54.8	2.7	366	1	Q49601	Human VEGF-121 cod
23	54.8	2.7	498	1	Q44260	Human VEGF-165 cod
24	53.2	2.7	366	1	Q11099	Human vascular end
25	53.2	2.7	456	1	T17740	VEGF121 Cys+2 codi
26	53.2	2.7	467	1	T17739	VEGF121 Cys+4 codi
27	53.2	2.7	473	1	Q99080	cDNA encoding huma
28	53.2	2.7	473	1	T17613	VEGF121 coding seq
29	53.2	2.7	498	1	Q10797	Human vascular end
30	53.2	2.7	516	1	V28396	Vascular endotheli
31	53.2	2.7	576	1	T95839	DNA for vascular e
32	53.2	2.7	599	1	T17747	VEGF165 Cys+4 codi
33	53.2	2.7	599	1	T17748	VEGF165 Cys+2 codi
34	53.2	2.7	605	1	Q99081	cDNA encoding huma
35	53.2	2.7	605	1	T17614	VEGF165 coding seq
36	53.2	2.7	649	1	T33609	Vascular endotheli
37	53.2	2.7	677	1	Q99082	cDNA encoding huma
38	53.2	2.7	677	1	T17615	VEGF189 coding seq
39	53.2	2.7	728	1	Q99083	cDNA encoding huma
40	53.2	2.7	728	1	T17616	VEGF206 coding seq
41	53.2	2.7	774	1	T10120	Vascular endotheli
42	53.2	2.7	774	1	T79139	Human vascular end
43	53.2	2.7	774	1	T85644	Antisense inhibito
44	53.2	2.7	774	1	T95393	Human vascular end
45	53.2	2.7	774	1	V15102	Human vascular end

ALIGNMENTS

RESULT 1
V15156
ID V15156 standard; cDNA to mRNA; 2004 BP.
AC V15156;
DT 22-JUN-1998 (first entry)
DE Human vascular endothelial growth factor D encoding cDNA.
KW Human; vascular endothelial growth factor D; VEGF-D; gene therapy;
KW inflammation; oedema; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 403. .1467
FT /*tag= a
FT /product= "VEGF-D"
PN WO9802543-A1.
PD 22-JAN-1998.
PF 15-JUL-1997; J02456.
PR 15-JUL-1996; JP-185216.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PI Hirata Y, Nezu J;
DR WPI; 98-110591/10.
DR P-PSDB; W44293.
PT VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT treating oedema
PS Claim 2; Page 21-24; 52pp; Japanese.
CC The present sequence encodes human vascular endothelial growth factor D
CC (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC the protein, may be useful in, e.g. gene therapy and in treatment of
CC inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
CC DNA sequences may be used for screening for the compounds which bind to
CC the VEGF-D protein.
SQ Sequence 2004 BP; 551 A; 441 C; 430 G; 579 T;

Query Match 99.9%; Score 2002.8; DB 1; Length 2004;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ccagctttctgtarctgtaagcattggtggccacaccacctccttacaaagcaactagaa 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCAGCTTTCTGTARCTGTAAGCATTGGTGGCCACACCACCTCCTTACAAAGCAACTAGAA 60

Qy     61 cctgcggcatacattggagagatttttttaattttctggacaygaagtaaatttagagtg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGCGGCATACATTGGAGAGATTTTTTTAATTTTCTGGACAYGAAGTAAATTTAGAGTG 120

Qy    121 ctttcyaatttcaggtagaagacatgtccaccttctgattatttttggagaacattttga 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTTTCYAATTTCAGGTAGAAGACATGTCCACCTTCTGATTATTTTTGGAGAACATTTTGA 180

Qy    181 ttttttttcatctctctctccccaccccctaagattgtgcaaaaaaaagcgtaccttgcctaa 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTTTTTTCATCTCTCTCTCCCCACCCCTAAGATTGTGCAAAAAAAGCGTACCTTGCCTAA 240

Qy    241 ttgaaataatttcattggattttgatcagaactgatcatttggttttctgtgtgaagttt 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTGAAATAATTTCATTGGATTTTGATCAGAACTGATCATTTGGTTTTCTGTGTGAAGTTT 300
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Qy    301 tgaggtttcaaactttccttctggagaatgccttttgaaacaattttctctagctgcctg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGAGGTTTCAAACTTTCCTTCTGGAGAATGCCTTTTGAAACAATTTTCTCTAGCTGCCTG 360

Qy    361 atgtcaactgcttagtaatcagtggatattgaaatattcaaaatgtacagagagtgggta 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGTCAACTGCTTAGTAATCAGTGGATATTGAAATATTCAAAATGTACAGAGAGTGGGTA 420

Qy    421 gtggtgaatgttttcatgatgttgtacgtccagctggtgcagggctccagtaatgaacat 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTGCAGGGCTCCAGTAATGAACAT 480

Qy    481 ggaccagtgaagcgatcatctcagtccacattggaacgatctgaacagcagatcagggct 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGACCAGTGAAGCGATCATCTCAGTCCACATTGGAACGATCTGAACAGCAGATCAGGGCT 540

Qy    541 gcttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggaga 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCTTCTAGTTTGGAGGAACTACTTCGAATTACTCACTCTGAGGACTGGAAGCTGTGGAGA 600

Qy    601 tgcaggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtcc 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGCAGGCTGAGGCTCAAAAGTTTTACCAGTATGGACTCTCGCTCAGCATCCCATCGGTCC 660

Qy    661 actaggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatgg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACTAGGTTTGCGGCAACTTTCTATGACATTGAAACACTAAAAGTTATAGATGAAGAATGG 720

Qy    721 caaagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaag 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAAAGAACTCAGTGCAGCCCTAGAGAAACGTGCGTGGAGGTGGCCAGTGAGCTGGGGAAG 780

Qy    781 agtaccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGTACCAACACATTCTTCAAGCCCCCTTGTGTGAACGTGTTCCGATGTGGTGGCTGTTGC 840

Qy    841 aatgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttt 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AATGAAGAGAGCCTTATCTGTATGAACACCAGCACCTCGTACATTTCCAAACAGCTCTTT 900

Qy    901 gagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcat 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAGATATCAGTGCCTTTGACATCAGTACCTGAATTAGTGCCTGTTAAAGTTGCCAATCAT 960

Qy    961 acaggttgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatcc 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACAGGTTGTAAGTGCTTGCCAACAGCCCCCCGCCATCCATACTCAATTATCAGAAGATCC 1020

Qy   1021 atccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatg 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATCCAGATCCCTGAAGAAGATCGCTGTTCCCATTCCAAGAAACTCTGTCCTATTGACATG 1080

Qy   1081 ctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaaca 1140
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Db   1081 CTATGGGATAGCAACAAATGTAAATGTGTTTTGCAGGAGGAAAATCCACTTGCTGGAACA 1140

Qy   1141 gaagaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaa 1200
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Db   1141 GAAGACCACTCTCATCTCCAGGAACCAGCTCTCTGTGGGCCACACATGATGTTTGACGAA 1200

Qy   1201 gatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaa 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GATCGTTGCGAGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAATCCAGCACCCCAAA 1260

Qy   1261 aactgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AACTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCTGCCAGAAGCACAAGCTA 1320

Qy   1321 tttcacccagacacctgcagctgtgaggacagatgccccctttcataccagaccatgtgca 1380
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Db   1321 TTTCACCCAGACACCTGCAGCTGTGAGGACAGATGCCCCTTTCATACCAGACCATGTGCA 1380

Qy   1381 agtggcaaaacagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccag 1440
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Db   1381 AGTGGCAAAACAGCATGTGCAAAGCATTGCCGCTTTCCAAAGGAGAAAAGGGCTGCCCAG 1440

Qy   1441 gggccccacagccgaaagaatccttgattcagcgttccaagttccccatccctgtcattt 1500
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Db   1441 GGGCCCCACAGCCGAAAGAATCCTTGATTCAGCGTTCCAAGTTCCCCATCCCTGTCATTT 1500

Qy   1501 ttaacagcatgctgctttgccaagttgctgtcactgtttttttcccaggtgttaaaaaaa 1560
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Db   1501 TTAACAGCATGCTGCTTTGCCAAGTTGCTGTCACTGTTTTTTTCCCAGGTGTTAAAAAAA 1560

Qy   1561 aaatccatttttacacagcaccacagtgaatccagaccaaccttccattcacaccagctaa 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 AAATCCATTTTACACAGCACCACAGTGAATCCAGACCAACCTTCCATTCACACCAGCTAA 1620

Qy   1621 ggagtccctggttcattgatggatgtcttctagctgcagatgcctctgcgcaccaaggaa 1680
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Db   1621 GGAGTCCCTGGTTCATTGATGGATGTCTTCTAGCTGCAGATGCCTCTGCGCACCAAGGAA 1680

Qy   1681 tggagaggaggggacccatgtaatccttttgtttagttttgtttttgttttttggtgaat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGGAGAGGAGGGGACCCATGTAATCCTTTTGTTTAGTTTTGTTTTTGTTTTTTGGTGAAT 1740

Qy   1741 gagaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattactcagagcagat 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GAGAAAGGTGTGCTGGTCATGGAATGGCAGGTGTCATATGACTGATTACTCAGAGCAGAT 1800

Qy   1801 gaggaaaactgtagtctctgagtcctttgctaatcgcaactcttgtgaattattctgatt 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAGGAAAACTGTAGTCTCTGAGTCCTTTGCTAATCGCAACTCTTGTGAATTATTCTGATT 1860

Qy   1861 ctttttatgcagaatttgattcgtatgatcagtactgactttctgattactgtccagct 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CTTTTTATGCAGAATTTGATTCGTATGATCAGTACTGACTTTCTGATTACTGTCCAGCT 1920

Qy   1921 tatagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtatttaaaga 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTATTTAAAGA 1980

Qy   1981 aaataaacaccattattcaagtct 2004
          |||||||||||||||||||||||
Db   1981 AAATAAACACCATTATTCAAGTCT 2004
```

RESULT 2
V20807
ID V20807 standard; cDNA; 2029 BP.
AC V20807;
DT 03-AUG-1998 (first entry)
DE Homo sapiens vascular endothelial growth factor D (VEGF-D) gene.
KW vascular endothelial growth factor; VEGF-D; angiogenesis;
KW modification; acceleration; wound healing; tissue; organ;
KW transplants; collateral circulation; infarction; arterial stenosis;
KW coronary artery disease; inhibition; cancer; treatment;
KW diabetic retinopathy; lung disorders; blood circulation;
KW gaseous exchange; chronic obstructive airway disease;
KW intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW detection; diagnosis; congestive heart failure; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 411. .1475
FT /*tag= a
FT /product= VEGF-D
FT /note= "isolated from lung tissue"
PN WO9807832-A1.
PD 26-FEB-1998.
PF 21-AUG-1997; U14696.
PR 01-JUL-1997; US-051426.
PR 23-AUG-1996; AU-001825.
PR 23-AUG-1996; US-023751.
PR 11-NOV-1996; AU-003554.
PR 14-NOV-1996; US-031097.
PR 05-FEB-1997; AU-004954.

PR 10-FEB-1997; US-038814.
PR 19-JUN-1997; AU-007435.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
PI Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR WPI; 98-179057/16.
DR P-PSDB; W53241.
PT New isolated vascular endothelial growth factor-D - used to develop
PT products for use in e.g. modifying angiogenesis or treating lung,
PT heart or intestinal disorders
PS Claim 6; Pages 58-59; 101pp; English.
CC The sequence is that encoding human vascular endothelial growth factor
CC D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis
CC in wound healing, tissue or organ transplantation, or to establish
CC collateral circulation in tissue infarction or arterial stenosis,
CC such as coronary artery disease, and inhibition of angiogenesis in
CC the treatment of cancer or of diabetic retinopathy. It can also be
CC used in the treatment of lung disorders to improve blood circulation
CC in the lung and/or gaseous exchange between the lungs and the blood
CC stream or to improve blood circulation to the heart and O2 gas
CC permeability in cases of cardiac insufficiency, to improve blood
CC flow and gaseous exchange in chronic obstructive airway disease,
CC or to treat malabsorptive syndromes in the intestinal tract.
CC Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC as an indicator of future metastatic risk. Antagonists can be used
CC for treating e.g. conditions such as congestive heart failure,
CC involving accumulations of fluid in the lung resulting from
CC increases in vascular permeability. The products can also be used
CC for detection and diagnosis.
SQ Sequence 2029 BP; 569 A; 441 C; 435 G; 584 T;

Query Match 99.7%; Score 1998.6; DB 1; Length 2029;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1998; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ccagctttctgtarctgtaagcattggtggccacaccacctccttacaaagcaactagaa 60
          ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 CCAGCTTTCTGTAGCTGTAAGCATTGGTGGCCACACCACCTCCTTACAAAGCAACTAGAA 68

Qy     61 cctgcggcatacattggagagatttttttaattttctggacaygaagtaaatttagagtg 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db     69 CCTGCGGCATACATTGGAGAGATTTTTTTAATTTTCTGGACATGAAGTAAATTTAGAGTG 128

Qy    121 ctttcyaatttcaggtagaagacatgtccaccttctgattatttttggagaacattttga 180
          |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 CTTTCTAATTTCAGGTAGAAGACATGTCCACCTTCTGATTATTTTTGGAGAACATTTTGA 188

Qy    181 ttttttcatctctctctccccaccccctaagattgtgcaaaaaaagcgtaccttgcctaa 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 TTTTTTTCATCTCTCTCTCCCCACCCCTAAGATTGTGCAAAAAAAGCGTACCTTGCCTAA 248

Qy    241 ttgaaataatttcattggattttgatcagaactgatcatttggttttctgtgtgaagttt 300
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    249 TTGAAATAATTTCATTGGATTTTGATCAGAACTGATTATTTGGTTTTCTGTGTGAAGTTT 308

Qy    301 tgaggtttcaaactttccttctggagaatgccttttgaaacaattttctctagctgcctg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 TGAGGTTTCAAACTTTCCTTCTGGAGAATGCCTTTTGAAACAATTTTCTCTAGCTGCCTG 368

Qy    361 atgtcaactgcttagtaatcagtggatattgaaatattcaaaatgtacagagagtgggta 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 ATGTCAACTGCTTAGTAATCAGTGGATATTGAAATATTCAAAATGTACAGAGAGTGGGTA 428

Qy    421 gtggtgaatgttttcatgatgttgtacgtccagctggtgcagggctccagtaatgaacat 480
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Db    429 GTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTGCAGGGCTCCAGTAATGAACAT 488

Qy    481 ggaccagtgaagcgatcatctcagtccacattggaacgatctgaacagcagatcagggct 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 GGACCAGTGAAGCGATCATCTCAGTCCACATTGGAACGATCTGAACAGCAGATCAGGGCT 548

Qy    541 gcttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggaga 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 GCTTCTAGTTTGGAGGAACTACTTCGAATTACTCACTCTGAGGACTGGAAGCTGTGGAGA 608

Qy    601 tgcaggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtcc 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 TGCAGGCTGAGGCTCAAAAGTTTTACCAGTATGGACTCTCGCTCAGCATCCCATCGGTCC 668

Qy    661 actaggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatgg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 ACTAGGTTTGCGGCAACTTTCTATGACATTGAAACACTAAAAGTTATAGATGAAGAATGG 728

Qy    721 caaagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaag 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 CAAAGAACTCAGTGCAGCCCTAGAGAAACGTGCGTGGAGGTGGCCAGTGAGCTGGGGAAG 788

Qy    781 agtaccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 AGTACCAACACATTCTTCAAGCCCCCTTGTGTGAACGTGTTCCGATGTGGTGGCTGTTGC 848

Qy    841 aatgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttt 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 AATGAAGAGAGCCTTATCTGTATGAACACCAGCACCTCGTACATTTCCAAACAGCTCTTT 908

Qy    901 gagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcat 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 GAGATATCAGTGCCTTTGACATCAGTACCTGAATTAGTGCCTGTTAAAGTTGCCAATCAT 968

Qy    961 acaggttgtaagtgcttgccaacagcccccgccatccatactcaattatcagaagatcc 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 ACAGGTTGTAAGTGCTTGCCAACAGCCCCCCGCCATCCATACTCAATTATCAGAAGATCC 1028

Qy   1021 atccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatg 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 ATCCAGATCCCTGAAGAAGATCGCTGTTCCCATTCCAAGAAACTCTGTCCTATTGACATG 1088

Qy   1081 ctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaaca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 CTATGGGATAGCAACAAATGTAAATGTGTTTTGCAGGAGGAAAATCCACTTGCTGGAACA 1148

Qy   1141 gaagaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaa 1200
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Db   1149 GAAGACCACTCTCATCTCCAGGAACCAGCTCTCTGTGGGCCACACATGATGTTTGACGAA 1208

Qy   1201 gatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaa 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 GATCGTTGCGAGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAATCCAGCACCCCAAA 1268

Qy   1261 aactgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 AACTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCTGCCAGAAGCACAAGCTA 1328

Qy   1321 tttcacccagacacctgcagctgtgaggacagatgccccctttcataccagaccatgtgca 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 TTTCACCCAGACACCTGCAGCTGTGAGGACAGATGCCCCTTTCATACCAGACCATGTGCA 1388

Qy   1381 agtggcaaaacagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccag 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 AGTGGCAAAACAGCATGTGCAAAGCATTGCCGCTTTCCAAAGGAGAAAAGGGCTGCCCAG 1448

Qy   1441 gggccccacagccgaaagaatccttgattcagcgttccaagttccccatccctgtcattt 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 GGGCCCCACAGCCGAAAGAATCCTTGATTCAGCGTTCCAAGTTCCCCATCCCTGTCATTT 1508

Qy   1501 ttaacagcatgctgctttgccaagttgctgtcactgtttttttcccaggtgttaaaaaaa 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TTAACAGCATGCTGCTTTGCCAAGTTGCTGTCACTGTTTTTTTCCCAGGTGTTAAAAAAA 1568

Qy   1561 aaatccattttacacagcaccacagtgaatccagaccaaccttccattcacaccagctaa 1620
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Db   1569 AAATCCATTTTACACAGCACCACAGTGAATCCAGACCAACCTTCCATTCACACCAGCTAA 1628

Qy   1621 ggagtccctggttcattgatggatgtcttctagctgcagatgcctctgcgcaccaaggaa 1680
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Db   1629 GGAGTCCCTGGTTCATTGATGGATGTCTTCTAGCTGCAGATGCCTCTGCGCACCAAGGAA 1688

Qy   1681 tggagaggaggggacccatgtaatccttttgtttagttttgtttttgtttttttggtgaat 1740
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Qy   1741 gagaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattactcagagcagat 1800
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Db   1749 GAGAAAGGTGTGCTGGTCATGGAATGGCAGGTGTCATATGACTGATTACTCAGAGCAGAT 1808

Qy   1801 gaggaaaactgtagtctctgagtcctttgctaatcgcaactcttgtgaattattctgatt 1860
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Db   1809 GAGGAAAACTGTAGTCTCTGAGTCCTTTGCTAATCGCAACTCTTGTGAATTATTCTGATT 1868

Qy   1861 ctttttttatgcagaatttgattcgtatgatcagtactgactttctgattactgtccagct 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 CTTTTTTATGCAGAATTTGATTCGTATGATCAGTACTGACTTTCTGATTACTGTCCAGCT 1928

Qy   1921 tatagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtatttaaaga 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 TATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTATTTAAAGA 1988

Qy   1981 aaataaacaccattattcaagtc 2003
          ||||||||||||||||||||| |
Db   1989 AAATAAACACCATTATTCAAGCC 2011


RESULT   3
T62961
ID   T62961 standard; DNA; 1864 BP.
AC   T62961;
DT   05-JUL-1997  (first entry)
DE   Human c-Fos induced growth factor gene HF175.
KW   c-Fos induced frowth factor; FIGF; Fos regulated gene;
KW   proto-oncogene; lung disorder; pneumonia; pneumoconiosis;
KW   gene therapy; antisense; ribozyme; cancer; proliferative disorder;
KW   transgenic animal; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             227. .229
FT                   /*tag= a
FT                   /transl_except= pos:227. .229:aa_Glu
FT                   /note= "ATT (reading frame 2) codes for Ile"
FT   cds             407. .409
FT                   /*tag= b
FT                   /transl_except= pos:407. .409:aa_Thr
FT                   /note= "ATT (reading frame 2) codes for Ile"
FT   cds             659. .661
FT                   /*tag= c
FT                   /transl_except= pos:659. .661:aa_Glu
FT                   /note= "TTC (reading frame 2) codes for Phe"
FT   cds             1022. .1024
FT                   /*tag= d
FT                   /transl_except= pos:1022. .1024:aa_Asp
FT                   /note= "CAC (reading frame 2) codes for His"
FT   cds             1031. .1033
FT                   /*tag= e
FT                   /transl_except= pos:1031. .1033:aa_Asp
FT                   /note= "TTT (reading frame 2) codes for Phe"
FT   cds             1130. .1132
FT                   /*tag= f
FT                   /transl_except= pos:1130. .1132:aa_Glu
FT                   /note= "CTG (reading frame 2) codes for Leu"
PN   WO9712972-A2.
PD   10-APR-1997.
PF   30-SEP-1996; IB1113.
PR   29-SEP-1995; GB-019928.
PR   13-JUN-1996; GB-012368.
PA   (UYSI-) UNIV SIENA.
PI   Oliviero S;
DR   WPI; 97-226216/20.
DR   P-PSDB; W14993;
DR   P-PSDB; W14994;
DR   P-PSDB; W14995.
PT   Nucleotide molecule encoding c-Fos induced growth factor protein -
PT   useful in therapy, in manufacture of compositions for treatment of
PT   developmental disorders and in generation of transgenic animal
PS   Claim 1; Fig 2; 64pp; English.
CC   Novel Fos regulated gene clone HF175 (T62961) codes for a human
CC   c-Fos induced growth factor (FIGF).  The nucleotide sequence has
CC   been mapped to human chromosome Xp22, near the locus for
CC   spondyloepiphyseal dysplasia.  HF175 is the human homologue of
CC   murine FIGF clone F-401 (see also T62960).  Translated amino acid
CC   sequences for FIGF are provided for all 3 reading frames of HF175
CC   (W14993-95); reading frame 2 provides the longest sequence
CC   uninterrupted by stop codons.  F0401 and HF175 are mainly expressed
CC   in the lungs.  They can be used in treatment of developmental
CC   disorders and may be used to treat lung disorders such as pneumonia
CC   and pneumoconiosis, or to aid lung re-growth after pneumonectomy.
CC   Antisense or ribozyme constructs can be used in the treatment of
CC   proliferative disorders, esp. cancer.  Transgenic animals can be
CC   generated e.g. as models for research.  Recombinant FIGF can be
CC   produced in transformed host (e.g. CHO) cells.
SQ   Sequence   1864 BP;    523 A;    405 C;    402 G;    534 T;


  Query Match             90.7%;  Score 1817.8;  DB 1;  Length 1864;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1822;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    175 ttttgatttttttcatctctctctccccacccctaagattgtgcaaaaaaagcgtaccttt 234
          ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     14 TTTTTTTTTTTTTCATCTCTCTCTCCCCACCCCTAAGATTGTGCAAAAAAAGCGTACCTT 73

Qy    235 gcctaattgaaataatttcattggattttgatcagaactgatcatttggttttctgtgtg 294
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     74 GCCTAATTGAAATAATTTCATTGGATTTTGATCAGAACTGATTATTTGGTTTTCTGTGTG 133

Qy    295 aagttttgaggtttcaaactttccttctggagaatgccttttgaaacaatttttctctagc 354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 AAGTTTTGAGGTTTCAAACTTTCCTTCTGGAGAATGCCTTTTGAAACAATTTTCTCTAGC 193

Qy    355 tgcctgatgtcaactgcttagtaatcagtggatattgaaatattcaaaatgtacagagag 414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 TGCCTGATGTCAACTGCTTAGTAATCAGTGGATATTGAAATATTCAAAATGTACAGAGAG 253

Qy    415 tgggtagtggtgaatgttttcatgatgttgtacgtccagctggtgcagggctccagtaat 474
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 TGGGTAGTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTGCAGGGCTCCAGTAAT 313

Qy    475 gaacatggaccagtgaagcgatcatctcagtccacattggaacgatctgaacagcagatc 534
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 GAACATGGACCAGTGAAGCGATCATCTCAGTCCACATTGGAACGATCTGAACAGCAGATC 373

Qy    535 agggctgcttctagtttggaggaactacttcgaattactcactctgaggactggaagctg 594
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 AGGGCTGCTTCTAGTTTGGAGGAACTACTTCGAATTACTCACTCTGAGGACTGGAAGCTG 433

Qy    595 tggagatgcaggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccat 654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 TGGAGATGCAGGCTGAGGCTCAAAAGTTTTACCAGTATGGACTCTCGCTCAGCATCCCAT 493

Qy    655 cggtccactaggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaa 714
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 CGGTCCACTAGGTTTGCGGCAACTTTCTATGACATTGAAACACTAAAAGTTATAGATGAA 553

Qy    715 gaatggcaaagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctg 774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 GAATGGCAAAGAACTCAGTGCAGCCCTAGAGAAACGTGCGTGGAGGTGGCCAGTGAGCTG 613

Qy    775 gggaagagtaccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggc 834
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 GGGAAGAGTACCAACACATTCTTCAAGCCCCCTTGTGTGAACGTGTTCCGATGTGGTGGT 673

Qy    835 tgttgcaatgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacag 894
          |||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||
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Db     674 TGTTGCAATGAAGAGAGCTTTATGTGTATGAACACCAGCACCTCGTACATTTCCAAACAG 733

Qy     895 ctctttgagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgcc 954
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     734 CTCTTTGAGATATCAGTGCCTTTGACATCAGTACCTGAATTAGTGCCTGTTAAAGTTGCC 793

Qy     955 aatcatacaggttgtaagtgcttgccaacagccccccgccatccatactcaattatcaga 1014
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     794 AATCATACAGGTTGTAAGTGCTTGCCAACAGCCCCCCGCCATCCATACTCAATTATCAGA 853

Qy    1015 agatccatccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctatt 1074
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     854 AGATCCATCCAGATCCCTGAAGAAGATCGCTGTTCCCATTCCAAGAAACTCTGTCCTATT 913

Qy    1075 gacatgctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgct 1134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     914 GACATGCTATGGGATAGCAACAAATGTAAATGTGTTTTGCAGGAGGAAAATCCACTTGCT 973

Qy    1135 ggaacagaagaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttt 1194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     974 GGAACAGAAGACCACTCTCATCTCCAGGAACCAGCTCTCTGTGGGCCACACATGATGTTT 1033

Qy    1195 gacgaagatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcac 1254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1034 GACGAAGATCGTTGCGAGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAATCCAGCAC 1093

Qy    1255 cccaaaaactgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcac 1314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1094 CCCAAAAACTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCTGCCAGAAGCAC 1153

Qy    1315 aagctatttcacccagacacctgcagctgtgaggacagatgccccctttcataccagacca 1374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1154 AAGCTATTTCACCCAGACACCTGCAGCTGTGAGGACAGATGCCCCTTTCATACCAGACCA 1213

Qy    1375 tgtgcaagtggcaaaacagcatgtgcaaagcattgccgctttccaaaggagaaaagggct 1434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1214 TGTGCAAGTGGCAAAACAGCATGTGCAAAGCATTGCCGCTTTCCAAAGGAGAAAAGGGCT 1273

Qy    1435 gcccaggggccccacagccgaaagaatccttgattcagcgttccaagttccccatccctg 1494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1274 GCCCAGGGGCCCCACAGCCGAAAGAATCCTTGATTCAGCGTTCCAAGTTCCCCATCCCTG 1333

Qy    1495 tcatttttaacagcatgctgctttgccaagttgctgtcactgtttttttcccaggtgtta 1554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1334 TCATTTTTAACAGCATGCTGCTTTGCCAAGTTGCTGTCACTGTTTTTTTCCCAGGTGTTA 1393

Qy    1555 aaaaaaaaatccattttacacagcaccacagtgaatccagaccaaccttccattcacacc 1614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1394 AAAAAAAAATCCATTTTACACAGCACCACAGTGAATCCAGACCAACCTTCCATTCACACC 1453

Qy    1615 agctaaggagtccctggttcattgatggatgtcttctagctgcagatgcctctgcgcacc 1674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1454 AGCTAAGGAGTCCCTGGTTCATTGATGGATGTCTTCTAGCTGCAGATGCCTCTGCGCACC 1513

Qy    1675 aaggaatggagaggaggggacccatgtaatccttttgtttagttttgtttttgttttttg 1734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1514 AAGGAATGGAGAGGAGGGGACCCATGTAATCCTTTTGTTTAGTTTTGTTTTTGTTTTTTG 1573

Qy    1735 gtgaatgagaaaggtgtgctggtcatggaatggcaggtgtcatatgactgattactcaga 1794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1574 GTGAATGAGAAAGGTGTGCTGGTCATGGAATGGCAGGTGTCATATGACTGATTACTCAGA 1633

Qy    1795 gcagatgaggaaaactgtagtctctgagtcctttgctaatcgcaactcttgtgaattatt 1854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1634 GCAGATGAGGAAAACTGTAGTCTCTGAGTCCTTTGCTAATCGCAACTCTTGTGAATTATT 1693

Qy    1855 ctgattctttttatgcagaatttgattcgtatgatcagtactgactttctgattactgt 1914
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1694 CTGATTCTTTTTTATGCAGAATTTGATTCGTATGATCAGTACTGACTTTCTGATTACTGT 1753

Qy    1915 ccagcttatagtcttccagtttaatgaactaccatctgatgtttcatatttaagtgtatt 1974
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1754 CCAGCTTATAGTCTTCCAGTTTAATGAACTACCATCTGATGTTTCATATTTAAGTGTATT 1813
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Qy    1975 taaagaaaataaacaccattattcaagtc 2003
           ||||||||||||||||||||||||||| |
Db    1814 TAAAGAAAATAAACACCATTATTCAAGCC 1842


RESULT   4
V20806
ID   V20806 standard; cDNA; 2846 BP.
AC   V20806;
DT   03-AUG-1998  (first entry)
DE   Homo sapiens vascular endothelial growth factor D (VEGF-D) gene.
KW   vascular endothelial growth factor; VEGF-D; angiogenesis;
KW   modification; acceleration; wound healing; tissue; organ;
KW   transplants; collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW   detection; diagnosis; congestive heart failure; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1771. .2748
FT                   /*tag=  a
FT                   /product= VEGF-D
FT                   /note= "isolated from breast tissue"
PN   WO9807832-A1.
PD   26-FEB-1998.
PF   21-AUG-1997; U14696.
PR   01-JUL-1997; US-051426.
PR   23-AUG-1996; AU-001825.
PR   23-AUG-1996; US-023751.
PR   11-NOV-1996; AU-003554.
PR   14-NOV-1996; US-031097.
PR   05-FEB-1997; AU-004954.
PR   10-FEB-1997; US-038814.
PR   19-JUN-1997; AU-007435.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR   WPI; 98-179057/16.
DR   P-PSDB; W53240.
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung,
PT   heart or intestinal disorders
PS   Claim 6; Pages 55-57; 101pp; English.
CC   The sequence is that encoding human vascular endothelial growth factor
CC   D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis
CC   in wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis,
CC   such as coronary artery disease, and inhibition of angiogenesis in
CC   the treatment of cancer or of diabetic retinopathy.  It can also be
CC   used in the treatment of lung disorders to improve blood circulation
CC   in the lung and/or gaseous exchange between the lungs and the blood
CC   stream or to improve blood circulation to the heart and O2 gas
CC   permeability in cases of cardiac insufficiency, to improve blood
CC   flow and gaseous exchange in chronic obstructive airway disease,
CC   or to treat malabsorptive syndromes in the intestinal tract.
CC   Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC   as an indicator of future metastatic risk. Antagonists can be used
CC   for treating e.g. conditions such as congestive heart failure,
CC   involving accumulations of fluid in the lung resulting from
CC   increases in vascular permeability.  The products can also be used
CC   for detection and diagnosis.
SQ   Sequence   2846 BP;    815 A;    636 C;    665 G;    730 T;


  Query Match             53.4%;  Score 1070.8;  DB 1;  Length 2846;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1072;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     490 aagcgatcatctcagtccacattggaacgatctgaacagcagatcagggctgcttctagt 549
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1771 ATGCGATCATCTCAGTCCACATTGGAACGATCTGAACAGCAGATCAGGGCTGCTTCTAGT 1830

Qy    550 ttggaggaactacttcgaattactcactctgaggactggaagctgtggagatgcaggctg 609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 TTGGAGGAACTACTTCGAATTACTCACTCTGAGGACTGGAAGCTGTGGAGATGCAGGCTG 1890

Qy    610 aggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtccactaggttt 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 AGGCTCAAAAGTTTTACCAGTATGGACTCTCGCTCAGCATCCCATCGGTCCACTAGGTTT 1950

Qy    670 gcggcaactttctatgacattgaaacactaaaagttatagatgaagaatggcaaagaact 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 GCGGCAACTTTCTATGACATTGAAACACTAAAAGTTATAGATGAAGAATGGCAAAGAACT 2010

Qy    730 cagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaagagtaccaac 789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 CAGTGCAGCCCTAGAGAAACGTGCGTGGAGGTGGCCAGTGAGCTGGGGAAGAGTACCAAC 2070

Qy    790 acattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgcaatgaagag 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 ACATTCTTCAAGCCCCCTTGTGTGAACGTGTTCCGATGTGGTGGCTGTTGCAATGAAGAG 2130

Qy    850 agccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttgagatatca 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AGCCTTATCTGTATGAACACCAGCACCTCGTACATTTCCAAACAGCTCTTTGAGATATCA 2190

Qy    910 gtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcatacaggttgt 969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 GTGCCTTTGACATCAGTACCTGAATTAGTGCCTGTTAAAGTTGCCAATCATACAGGTTGT 2250

Qy    970 aagtgcttgccaacagccccccgccatccatactcaattatcagaagatccatccagatc 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 AAGTGCTTGCCAACAGCCCCCCGCCATCCATACTCAATTATCAGAAGATCCATCCAGATC 2310

Qy   1030 cctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatgctatgggat 1089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 CCTGAAGAAGATCGCTGTTCCCATTCCAAGAAACTCTGTCCTATTGACATGCTATGGGAT 2370

Qy   1090 agcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaacagaagaccac 1149
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   2371 AGCAACAAATGTAAATGTGTTTTGCAGGAGGAAAATCCACTCGCTGGAACAGAAGACCAC 2430

Qy   1150 tctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaagatcgttgc 1209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 TCTCATCTCCAGGAACCAGCTCTCTGTGGGCCACACATGATGTTTGACGAAGATCGTTGC 2490

Qy   1210 gagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaaaactgcagt 1269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 GAGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAATCCAGCACCCCAAAAACTGCAGT 2550

Qy   1270 tgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagctatttcaccca 1329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 TGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCTGCCAGAAGCACAAGCTATTTCACCCA 2610

Qy   1330 gacacctgcagctgtgaggacagatgccccttcataccagaccatgtgcaagtggcaaa 1389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 GACACCTGCAGCTGTGAGGACAGATGCCCCTTTCATACCAGACCATGTGCAAGTGGCAAA 2670

Qy   1390 acagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccaggggccccac 1449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 ACAGCATGTGCAAAGCATTGCCGCTTTCCAAAGGAGAAAAGGGCTGCCCAGGGGCCCCAC 2730

Qy   1450 agccgaaagaatccttgattcagcgttccaagttccccatccctgtcatttttaacagca 1509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 AGCCGAAAGAATCCTTGATTCAGCGTTCCAAGTTCCCCATCCCTGTCATTTTTAACAGCA 2790

Qy   1510 tgctgctttgccaagttgctgtcactgtttttttcccaggtgttaaaaaaaaaa 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 TGCTGCTTTGCCAAGTTGCTGTCACTGTTTTTTTCCCAGGTGTTAAAAAAAAAA 2844


RESULT   5
V32823
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ID   V32823 standard; cDNA; 1107 BP.
AC   V32823;
DT   26-OCT-1998  (first entry)
DE   Human zvegf2 growth factor cDNA.
KW   Human zvegf2 growth factor; mitogen; fibroblast; smooth muscle cell;
KW   venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect;
KW   angiogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis;
KW   scleroderma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .1068
FT                   /*tag= a
FT                   /product= "Human zvegf2 protein"
FT                   /note= "CDS does not contain a stop codon"
PN   WO9824811-A2.
PD   11-JUN-1998.
PF   20-NOV-1997; U20888.
PR   18-SEP-1997; US-933455.
PR   06-DEC-1996; US-759657.
PA   (ZYMO ) ZYMOGENETICS INC.
PI   Conklin DC, Gilbert T, Hart CE, Nygaard S, Sheppard PO;
DR   WPI; 98-333256/29.
DR   P-PSDB; W49036.
PT   New isolated vascular endothelial growth factor - used to develop
PT   products for treating e.g. wounds, burns, myocardial infarction,
PT   tumours, psoriasis, arthritis, restenosis or organ transplants
PS   Example 1; Pages 50-53; 77pp; English.
CC   The present sequence represents a human zvegf2 cDNA isolated from a
CC   human heart cDNA library.  zvegf2 protein is a growth factor, which
CC   in its dimeric form acts as a mitogen for fibroblasts or smooth muscle
CC   cells.  zvegf2 is claimed to be useful for stimulating the
CC   revascularisation of tissue or the re-endothelialisation of vascular
CC   tissue.  zvefg2 is particularly claimed to be useful for the treatment
CC   of full-thickness skin wounds, including venous stasis ulcers and
CC   diabetic ulcers.  The zvegf2 protein is also claimed to be useful as an
CC   additive in tissue adhesives for promoting revascularisation of the
CC   healing tissue.  Antagonists against zvegf2 can be used to block its
CC   mitogenic, chemotactic and angiogenic effects.  The antagonists may
CC   therefore be useful for reducing growth of solid tumours by inhibiting
CC   neovascularisation of the developing tumour or by directly blocking
CC   tumour cell growth, in the treatment of diabetic retinopathy, psoriasis,
CC   arthritis, and scleroderma.
SQ   Sequence   1107 BP;    312 A;    272 C;    265 G;    258 T;


  Query Match             53.2%;  Score 1065.6;  DB 1;  Length 1107;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1068;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    403 atgtacagagagtgggtagtggtgaatgttttcatgatgttgtacgtccagctggtgcag 462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 ATGTACAGAGAGTGGGTAGTGGTGAATGTTTTCATGATGTTGTACGTCCAGCTGGTGCAG 66

Qy    463 ggctccagtaatgaacatggaccagtgaagcgatcatctcagtccacattggaacgatct 522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 GGCTCCAGTAATGAACATGGACCAGTGAAGCGATCATCTCAGTCCACATTGGAACGATCT 126

Qy    523 gaacagcagatcagggctgcttctagtttggaggaactacttcgaattactcactctgag 582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GAACAGCAGATCAGGGCTGCTTCTAGTTTGGAGGAACTACTTCGAATTACTCACTCTGAG 186

Qy    583 gactggaagctgtggagatgcaggctgaggctcaaaagttttaccagtatggactctcgc 642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 GACTGGAAGCTGTGGAGATGCAGGCTGAGGCTCAAAAGTTTTACCAGTATGGACTCTCGC 246

Qy    643 tcagcatcccatcggtccactaggtttgcggcaactttctatgacattgaaacactaaaa 702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TCAGCATCCCATCGGTCCACTAGGTTTGCGGCAACTTTCTATGACATTGAAACACTAAAA 306

Qy    703 gttatagatgaagaatggcaaagaactcagtgcagccctagagaaacgtgcgtggaggtg 762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GTTATAGATGAAGAATGGCAAAGAACTCAGTGCAGCCCTAGAGAAACGTGCGTGGAGGTG 366
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Qy     763 gccagtgagctggggaagagtaccaacacattcttcaagccccccttgtgtgaacgtgttc 822
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 GCCAGTGAGCTGGGGAAGAGTACCAACACATTCTTCAAGCCCCCTTGTGTGAACGTGTTC 426

Qy     823 cgatgtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcgtac 882
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 CGATGTGGTGGCTGTTGCAATGAAGAGAGCCTTATCTGTATGAACACCAGCACCTCGTAC 486

Qy     883 atttccaaacagctctttgagatatcagtgcctttgacatcagtacctgaattagtgcct 942
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 ATTTCCAAACAGCTCTTTGAGATATCAGTGCCTTTGACATCAGTACCTGAATTAGTGCCT 546

Qy     943 gttaaagttgccaatcatacaggttgtaagtgcttgccaacagccccccgccatccatac 1002
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 GTTAAAGTTGCCAATCATACAGGTTGTAAGTGCTTGCCAACAGCCCCCCGCCATCCATAC 606

Qy    1003 tcaattatcagaagatccatccagatccctgaagaagatcgctgttcccattccaagaaa 1062
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 TCAATTATCAGAAGATCCATCCAGATCCCTGAAGAAGATCGCTGTTCCCATTCCAAGAAA 666

Qy    1063 ctctgtcctattgacatgctatgggatagcaacaaatgtaaatgtgttttgcaggaggaa 1122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 CTCTGTCCTATTGACATGCTATGGGATAGCAACAAATGTAAATGTGTTTTGCAGGAGGAA 726

Qy    1123 aatccacttgctggaacagaagaccactctcatctccaggaaccagctctctgtgggcca 1182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 AATCCACTTGCTGGAACAGAAGACCACTCTCATCTCCAGGAACCAGCTCTCTGTGGGCCA 786

Qy    1183 cacatgatgtttgacgaagatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagat 1242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 CACATGATGTTTGACGAAGATCGTTGCGAGTGTGTCTGTAAAACACCATGTCCCAAAGAT 846

Qy    1243 ctaatccagcaccccaaaaactgcagttgctttgagtgcaaagaaagtctggagacctgc 1302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 CTAATCCAGCACCCCAAAAACTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGC 906

Qy    1303 tgccagaagcacaagctatttcacccagacacctgcagctgtgaggacagatgccccttt 1362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 TGCCAGAAGCACAAGCTATTTCACCCAGACACCTGCAGCTGTGAGGACAGATGCCCCTTT 966

Qy    1363 cataccagaccatgtgcaagtggcaaaacagcatgtgcaaagcattgccgctttccaaag 1422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 CATACCAGACCATGTGCAAGTGGCAAAACAGCATGTGCAAAGCATTGCCGCTTTCCAAAG 1026

Qy    1423 gagaaaagggctgcccaggggccccacagccgaaagaatccttgattcagcg 1474
           ||||||||||||||||||||||||||||||||||||||||||| ||| | | |
Db    1027 GAGAAAAGGGCTGCCCAGGGGCCCCACAGCCGAAAGAATCCTGGATCCGGTG 1078


RESULT   6
T62960
ID   T62960 standard; DNA; 1890 BP.
AC   T62960;
DT   05-JUL-1997  (first entry)
DE   Murine c-Fos induced growth factor gene F0401.
KW   c-Fos induced frowth factor; FIGF; Fos regulated gene;
KW   proto-oncogene; lung disorder; pneumonia; pneumoconiosis;
KW   gene therapy; antisense; ribozyme; cancer; proliferative disorder;
KW   transgenic animal; ss.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   cds             283. .1359
FT                   /*tag=  a
PN   WO9712972-A2.
PD   10-APR-1997.
PF   30-SEP-1996; IB1113.
PR   29-SEP-1995; GB-019928.
PR   13-JUN-1996; GB-012368.
PA   (UYSI-) UNIV SIENA.
PI   Oliviero S;
DR   WPI; 97-226216/20.
DR   P-PSDB; W14992.
PT   Nucleotide molecule encoding c-Fos induced growth factor protein -
PT   useful in therapy, in manufacture of compositions for treatment of
PT   developmental disorders and in generation of transgenic animal
PS   Claim 1; Fig 1; 64pp; English.
CC   Novel Fos regulated gene F0401 (T62960) codes for a murine c-Fos
CC   induced growth factor (FIGF) (W14992) that shows homology to the
CC   growth factor VEGF.  Mouse fibroblast cells wild-type for c-Fos
CC   expression, c-Fos-deficient 3T3 cells, and transfected cells that
CC   constitutively expressed exogenous c-Fos were subjected to mRNA
CC   differential display analysis, and full-length clones corresponding
CC   to mRNA sequences up-regulated in Fos-expressing clones were
CC   isolated from a mouse fibroblast cDNA library.  A human homologue,
CC   HF175 (see also T62961), was also isolated.  F0401 and HF175 are
CC   mainly expressed in the lungs.  They can be used in treatment of
CC   developmental disorders and may be used to treat lung disorders such
CC   as pneumonia and pneumoconiosis, or to aid lung re-growth after
CC   pneumonectomy.  Antisense or ribozyme constructs can be used in the
CC   treatment of proliferative disorders, esp. cancer.  Transgenic
CC   animals can be generated e.g. as models for research.  Recombinant
CC   FIGF can be produced in transformed host (e.g. CHO) cells.
SQ   Sequence   1890 BP;    511 A;    445 C;    431 G;    503 T;


  Query Match            48.8%;  Score 977;  DB 1;  Length 1890;
  Best Local Similarity  74.6%;  Pred. No. 3.6e-278;
  Matches 1434;  Conservative    0;  Mismatches  375;  Indels  112;  Gaps   12;

Qy     138 gaagacatgtccaccttctgattatttttggag-----aacattttgatttttttcatct 192
           ||||| ||| |||||| |||||||||||||| ||     ||| ||   || ||||||||
Db       2 GAAGATATGACCACCTCCTGATTATTTTTGCAGCGGGAAACTTTGAAATATTTTTCATTG 61

Qy     193 ctctctccccaccctaagattgt-----gcaaaaaaagcgtaccttgcctaattgaaat 247
           || |||||   |    |   |||     |||   |  | || ||||| || | | || |
Db      62 CTTTCTCCCATACTAAGATTGTGTGTGAGGCAGTGAGGGAGTCCCTTGACTTACTCAAGT 121

Qy     248 aatttcattggattttgatcagaactgatcatttggttttctgtgt-----gaagttttg 302
           ||||||||||||||| || | |||||||||| || || | | | |     ||  ||||
Db     122 CATTTCATTGGATTTTAATTACAACTGATCATGTGATTGTTTTTTTCCATGTAAAGTTTG 181

Qy     303 aggtttcaaactttccttctggagaatgccttttgaaacaattttctctagctgcctgat 362
           || |||||||||| ||||||||||||||||||||| |||| |||||  ||||||||||
Db     182 GGGCTTCAAACTTTGCTTCTGGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGA 241

Qy     363 gtcaactgcttagtaatcagtggata-ttgaaatattcaaaatgtacagagagtgggtag 421
           ||||||||||| ||| || || | || ||||||||||||||||  |||| |||| |
Db     242 AACAACTGCTTAGTCATCGGTAGACATTTAAAATATTCAAAATGTATGGAGAATGGGGAA 301

Qy     422 tggtgaatgttttcatgatgttgtacgtccagctggtgcagggctccagtaatgaacatg 481
           ||| |||| |  |||||||||| | ||  |  |||||||||||| ||| |  |||||||
Db     302 TGGGGAATATCCTCATGATGTTCCATGTGTACTTGGTGCAGGGCTTCAGGAGCGAACATG 361

Qy     482 gaccagtga----------------agcgatcatctcagtccacattggaacgatctgaac 526
           |||||||||                |||||||||| | |||||  ||||||||||||||||
Db     362 GACCAGTGAAGGATTTTTCTTTTGAGCGATCATCCCGGTCCATGTTGGAACGATCTGAAC 421

Qy     527 agcagatcagggctgcttctagtttggaggaactacttcgaattactcactctgaggact 586
           | |||||| | || |||||||||||||||||  | || | |||  | ||||||||||||
Db     422 AACAGATCCGAGCAGCTTCTAGTTTGGAGGAGTTGCTGCAAATCGCGCACTCTGAGGACT 481

Qy     587 ggaagctgtggagatgcaggctgaggctcaaaagttttaccagtatggactctcgctcag 646
           |||||||||| ||||| || ||| |||||||||| || |||||||||| || |||||||
Db     482 GGAAGCTGTGGCGATGCCGGTTGAAGCTCAAAAGTCTTGCCAGTATGGAATCACGCTCAG 541

Qy     647 catcccatcggtccactaggtttgcggcaactttctatgacattgaaacactaaaagtta 706
           |||||||||| ||||| || |||||||||||||||||||| ||||||||||||||||||
Db     542 CATCCCATCGCTCCACCAGATTTGCGGCAACTTTCTATGACACTGAAACACTAAAAGTTA 601

Qy     707 tagatgaagaatggcaaagaactcagtgcagccctagagaaacgtgcgtggaggtggcca 766
           |||||||||||||||| || || || |||||||||||||| || ||||| || || ||||
Db     602 TAGATGAAGAATGGCAGAGGACCCAATGCAGCCCTAGAGAGACATGCGTAGAAGTCGCCA 661

Qy     767 gtgagctggggaagagtaccaacacattcttcaagccccccttgtgtgaacgtgttccgat 826
           ||||||||||||||  ||||||||||||||||||||| ||||| || || ||||| |
Db     662 GTGAGCTGGGGAAGACAACCAACACATTCTTCAAGCCCCCCTGTGTAAATGTCTTCCGGT 721
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Qy    827 gtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcgtacattt 886
          |||| ||||| ||||| |||||| |  | || |||||||||| |||||||| ||||| |
Db    722 GTGGAGGCTGCTGCAACGAAGAGGGTGTGATGTGTATGAACACAAGCACCTCCTACATCT 781

Qy    887 ccaaacagctctttgagatatcagtgcctttgacatcagtacctgaattagtgcctgtta 946
          |||||||||||||||||||||||||||||| |||||||||| || || ||||||||||||
Db    782 CCAAACAGCTCTTTGAGATATCAGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTA 841

Qy    947 aagttgccaatcatacaggttgtaagtgcttgccaacagccccccgccatccatactcaa 1006
          || ||||||| ||||| |||||||||||||||||| || | ||||||||||| |||||||
Db    842 AAATTGCCAACCATACGGGTTGTAAGTGCTTGCCCACGGGCCCCCGCCATCCTTACTCAA 901

Qy   1007 ttatcagaagatccatccagatccctgaagaagatcgctgttcccattccaagaaactct 1066
          |||||||||||||||| |||| ||| |||||||||   ||| | ||||||||||||||||
Db    902 TTATCAGAAGATCCATTCAGACCCCAGAAGAAGATGAATGTCCTCATTCCAAGAAACTCT 961

Qy   1067 gtcctattgacatgctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatc 1126
          |||||||||||||||| ||||||| || |||||||||||||||||||| || || | ||
Db    962 GTCCTATTGACATGCTGTGGGATAACACCAAATGTAAATGTGTTTTGCAAGACGAGACTC 1021

Qy   1127 cacttgctggaacagaagaccactctcatctccaggaaccagctctctgtgggccacaca 1186
          ||||  |||| |||||||||||||||| | ||||||||||  |||||||||| || ||||
Db   1022 CACTGCCTGGGACAGAAGACCACTCTTACCTCCAGGAACCCACTCTCTGTGGACCGCACA 1081

Qy   1187 tgatgtttgacgaagatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaa 1246
          ||| |||||| |||||||| || ||||| |||||||| |||||||||   |||||| |
Db   1082 TGACGTTTGATGAAGATCGCTGTGAGTGCGTCTGTAAAGCACCATGTCCGGGAGATCTCA 1141

Qy   1247 tccagcaccccaaaaactgcagttgctttgagtgcaaagaaagtctggagacctgctgcc 1306
          | ||||||||  ||||||||||||||||||||||||||||||||||||||| ||||||||
Db   1142 TTCAGCACCCGGAAAACTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGAGCTGCTGCC 1201

Qy   1307 agaagcacaagctatttcacccagacacctgcagctgtgaggacagatgccccttttcata 1366
          | ||||||||| | |||||||||||||||||||||||||||||||||||||| || ||||| |
Db   1202 AAAAGCACAAGATTTTTCACCCAGACACCTGCAGCTGTGAGGACAGATGTCCTTTTCACA 1261

Qy   1367 ccagaccatgtgcaagtggcaaaacagcatgtgcaaagcattgccgctttccaaaggaga 1426
          ||||| |||||||||| | ||  |||| |||| |||||| || ||||||||||||||||
Db   1262 CCAGAACATGTGCAAGTAGAAAGCCAGCCTGTGGAAAGCACTGGCGCTTTCCAAAGGAGA 1321

Qy   1427 aaagggctgcccaggggccccacagccgaaagaatccttgattca----gcgttccaagt 1482
           ||||   |||||||| | | ||||||   |||| ||||||||||     | ||| |
Db   1322 CAAGG---GCCCAGGGACTCTACAGCCAGGAGAACCCTTGATTCAACTTCCTTTCAAGTC 1378

Qy   1483 tccccatccctgtcatttttaacagcatgctgctttgccaagttgctgtcactgtt---- 1539
          |||||||| |||||||||| ||||||   |||||||| ||||||||||||||||||
Db   1379 CCCCCATCTCTGTCATTTTAAACAGCTCACTGCTTTGTCAAGTTGCTGTCACTGTTGCCC 1438

Qy   1539 --------------------ttttcccaggtgttaaaaaaaaaatccattttacacagc 1578
                              |     ||    | |   | |||| |  |||| ||  ||
Db   1439 ACTACCCCTGCCCCCCCCCCTCCCCGCCTCCAGGTGTTAGAAAAGTTGATTTGACCTAGT 1498

Qy   1579 accacagtgaatccagaccaaccttccattcacaccagctaaggagtccctggttcattg 1638
           ||  || || ||| |    | | | ||     | || |   || ||||  ||||| ||
Db   1499 GTCATGGTAAAGCCACATTTCCATGCAATGGCGGCTAGGT---GATTCCCCAGTTCACTG 1555

Qy   1639 atggatgtcttctagctgcagatgcctctgcgcaccaaggaatggagaggaggggaccca 1698
          |   ||| ||| ||||| |||||| || |||||    || | |    | |   ||   |
Db   1556 ACAAATGACTTGTAGCTTCAGATGTCTTTGCGCCATCAGCACTCAGAAAGGAAGGGGTCT 1615

Qy   1699 tgtaatccttttgtttagttttgtttttgtttttggtgaatgagaaaggtgtgctggtc 1758
              | ||  |||                  ||||| ||||| ||||| |  |||  |
Db   1616 GAGGAGCCCCTTG------------------TTTTGATGAATAAGAAAAGGTTGCCTGAA 1657

Qy   1759 atggaatggcaggtgtcatatgactgattactcagagcagatgaggaaaactgtagtctc 1818
          |  || | | ||||| ||   || || || ||| |    |   ||
Db   1658 ACAGAGTAGTAGGTGCCACTCGATTGGTTCCTCGGGCTGGCAAAG--------------- 1703

Qy   1819 tgagtcctttgctaatcgcaactcttgtgaattattctgattctttttttatgcagaattt 1878
                  | ||  ||||  ||  ||| ||||| || |||||| |||||| ||||||
Db   1703 ----------TCCAAGGGCAATGCTCATGAGTTATTGTGCTTCTTTCTTATGCGGAATTT 1752
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Qy   1879 gattcgtatgatcagtactgactttctgattactgtccagcttatagtcttccagtttaa 1938
          ||| ||||||||||| |||||       ||| |  | |  ||| || | ||   |||||
Db   1753 CATTTGTATGATCAGCACTGA----TCAATTCCCATTCCACTTGTACTTTTTAGGTTTAC 1808

Qy   1939 tgaactaccatctgatgtttcatatttaagtgtatttaaagaaaataaacaccattattc 1998
          ||||  ||   ||||||||| |||| ||| |||||||||| ||||||||||  |||| |
Db   1809 TGAAGCACTGCCTGATGTTTTATATGTAAATGTATTTAAAGGAAATAAACACTGTTATGC 1868

Qy   1999 a 1999
          |
Db   1869 A 1869


RESULT   7
V15177
ID   V15177 standard; cDNA to mRNA; 1581 BP.
AC   V15177;
DT   22-JUN-1998  (first entry)
DE   Mouse vascular endothelial growth factor D encoding cDNA.
KW   Mouse; vascular endothelial growth factor D; VEGF-D; gene therapy;
KW   inflammation; oedema; ds.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   CDS             96. .1172
FT                   /*tag= a
FT                   /product= "VEGF-D"
PN   WO9802543-A1.
PD   22-JAN-1998.
PF   15-JUL-1997; J02456.
PR   15-JUL-1996; JP-185216.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PI   Hirata Y, Nezu J;
DR   WPI; 98-110591/10.
DR   P-PSDB; W44295.
PT   VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT   treating oedema
PS   Example 7; Page 32-35; 52pp; Japanese.
CC   The present sequence encodes mouse vascular endothelial growth factor D
CC   (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC   the protein, may be useful in, e.g. gene therapy and in treatment of
CC   inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
CC   DNA sequences may be used for screening for the compounds which bind to
CC   the VEGF-D protein.
SQ   Sequence   1581 BP;    420 A;    401 C;    367 G;    392 T;


  Query Match             43.8%;  Score 877.2;  DB 1;  Length 1581;
  Best Local Similarity   84.2%;  Pred. No. 8.9e-249;
  Matches 1044;  Conservative    0;  Mismatches  173;  Indels   23;  Gaps    4;

Qy    319 ttctggagaatgccttttgaaacaattttctctagctgcctgatgtcaactgcttagtaa 378
          | |||||||||||||||| |||| |||||  ||||||||||    |||||||||||| |
Db     11 TGCTGGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAGTCA 70

Qy    379 tcagtggata-ttgaaatattcaaaatgtacagagagtgggtagtggtgaatgttttcat 437
          || || || | || |||||||||||||||  |||| |||| | ||| |||| |  ||||
Db     71 TCGGTAGACATTTAAAATATTCAAAATGTATGGAGAATGGGGAATGGGGAATATCCTCAT 130

Qy    438 gatgttgtacgtccagctggtgcagggctccagtaatgaacatggaccagtga------- 491
          ||||||  | ||  |  |||||||||||| ||| |  ||||||||||||||||
Db    131 GATGTTCCATGTGTACTTGGTGCAGGGCTTCAGGAGCGAACATGGACCAGTGAAGGATTT 190

Qy    491 --------agcgatcatctcagtccacattggaacgatctgaacagcagatcagggctgc 542
                  |||||||||| | |||||  ||||||||||||||||| |||||| | || ||
Db    191 TTCTTTTGAGCGATCATCCCGGTCCATGTTGGAACGATCTGAACAACAGATCCGAGCAGC 250

Qy    543 ttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggagatg 602
          ||||||||||||||||  | || | |||  | |||||||||||||||||||||||| ||||
Db    251 TTCTAGTTTGGAGGAGTTGCTGCAAATCGCGCACTCTGAGGACTGGAAGCTGTGGCGATG 310

Qy    603 caggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtccac 662
          | || ||| |||||||||| || |||||||||||| |||||||||||||||| |||||
Db    311 CCGGTTGAAGCTCAAAAGTCTTGCCAGTATGGACTCACGCTCAGCATCCCATCGCTCCAC 370
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Qy     663 taggtttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatggca 722
           || ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     371 CAGATTTGCGGCAACTTTCTATGACACTGAAACACTAAAAGTTATAGATGAAGAATGGCA 430

Qy     723 aagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaagag 782
           || || || ||||||||||||||| || ||||| || || ||||||||||||||||||||
Db     431 GAGGACCCAATGCAGCCCTAGAGAGACATGCGTAGAAGTCGCCAGTGAGCTGGGGAAGAC 490

Qy     783 taccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgcaa 842
           |||||||||||||||||||||| ||||| || || ||||| ||||| ||||| |||||
Db     491 AACCAACACATTCTTCAAGCCCCCCTGTGTAAATGTCTTCCGGTGTGGAGGCTGCTGCAA 550

Qy     843 tgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttga 902
           ||||||  |  | || |||||||||||| |||||||| ||||| ||||||||||||||||
Db     551 CGAAGAGGGTGTGATGTGTATGAACACAAGCACCTCCTACATCTCCAAACAGCTCTTTGA 610

Qy     903 gatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcatac 962
           |||||||||||||| |||||||||| || || |||||||||||||| ||||||| |||||
Db     611 GATATCAGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTAAAATTGCCAACCATAC 670

Qy     963 aggttgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatccat 1022
           |||||||||||||||| || | |||||||||||| ||||||||||||||||||||||||
Db     671 GGGTTGTAAGTGCTTGCCCACGGGCCCCCGCCATCCTTACTCAATTATCAGAAGATCCAT 730

Qy    1023 ccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatgct 1082
           |||| ||| |||||||||   ||| | ||||||||||||||||||||||||||||||||
Db     731 TCAGACCCCAGAAGAAGATGAATGTCCTCATTCCAAGAAACTCTGTCCTATTGACATGCT 790

Qy    1083 atgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaacaga 1142
           ||||||| || |||||||||||||||||||| || || | ||||||  |||| ||||||
Db     791 GTGGGATAACACCAAATGTAAATGTGTTTTGCAAGACGAGACTCCACTGCCTGGGACAGA 850

Qy    1143 agaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaaga 1202
           |||||||||| | ||||||||||  |||||||||| || ||||||| |||||| ||||||
Db     851 AGACCACTCTTACCTCCAGGAACCCACTCTCTGTGGACCGCACATGACGTTTGATGAAGA 910

Qy    1203 tcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaaaa 1262
           ||| || ||||| ||||||||| |||||||||   |||||| || ||||||||  ||||
Db     911 TCGCTGTGAGTGCGTCTGTAAAGCACCATGTCCGGGAGATCTCATTCAGCACCCGGAAAA 970

Qy    1263 ctgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagctatt 1322
           |||||||||||||||||||||||||||||||| ||||||||| ||||||||  | ||
Db     971 CTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGAGCTGCTGCCAAAAGCACAAGATTTT 1030

Qy    1323 tcacccagacacctgcagctgtgaggacagatgccccttcataccagaccatgtgcaag 1382
           |||||||||||||||||||||||||||||||| || ||||| ||||||  ||||||||||
Db    1031 TCACCCAGACACCTGCAGCTGTGAGGACAGATGTCCTTTTCACACCAGAACATGTGCAAG 1090

Qy    1383 tggcaaaacagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccaggg 1442
           | | ||  |||| |||| |||||| || |||||||||||||||| ||||   ||||||||
Db    1091 TAGAAAGCCAGCCTGTGGAAAGCACTGGCGCTTTCCAAAGGAGACAAGG---GCCCAGGG 1147

Qy    1443 gccccacagccgaaagaatccttgattca----gcgttccaagttccccatccctgtcat 1498
           | | ||||||   |||| ||||||||||     | ||| |    ||||||| |||||||
Db    1148 ACTCTACAGCCAGGAGAACCCTTGATTCAACTTCCTTTCAAGTCCCCCCATCTCTGTCAT 1207

Qy    1499 ttttaacagcatgctgctttgccaagttgctgtcactgtt 1538
           ||| ||||||   |||||||| ||||||||||||||||||
Db    1208 TTTAAACAGCTCACTGCTTTGTCAAGTTGCTGTCACTGTT 1247


RESULT   8
V20808
ID   V20808 standard; cDNA; 1325 BP.
AC   V20808;
DT   03-AUG-1998  (first entry)
DE   Mus musculus vascular endothelial growth factor D1 (VEGF-D1) gene.
KW   vascular endothelial growth factor; VEGF-D; angiogenesis;
KW   modification; acceleration; wound healing; tissue; organ;
KW   transplants; collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW   detection; diagnosis; congestive heart failure; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             82. .1158
FT                   /*tag=  a
FT                   /product= VEGF-D1
FT                   /note= "isolated from lung tissue"
PN   WO9807832-A1.
PD   26-FEB-1998.
PF   21-AUG-1997; U14696.
PR   01-JUL-1997; US-051426.
PR   23-AUG-1996; AU-001825.
PR   23-AUG-1996; US-023751.
PR   11-NOV-1996; AU-003554.
PR   14-NOV-1996; US-031097.
PR   05-FEB-1997; AU-004954.
PR   10-FEB-1997; US-038814.
PR   19-JUN-1997; AU-007435.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR   WPI; 98-179057/16.
DR   P-PSDB; W53242.
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung,
PT   heart or intestinal disorders
PS   Claim 6; Pages 61-62; 101pp; English.
CC   The sequence is that encoding mouse vascular endothelial growth factor
CC   D1 (VEGF-D1). VEGF-D1 can be used for e.g. acceleration of angiogenesis
CC   in wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis,
CC   such as coronary artery disease, and inhibition of angiogenesis in
CC   the treatment of cancer or of diabetic retinopathy.  It can also be
CC   used in the treatment of lung disorders to improve blood circulation
CC   in the lung and/or gaseous exchange between the lungs and the blood
CC   stream or to improve blood circulation to the heart and O2 gas
CC   permeability in cases of cardiac insufficiency, to improve blood
CC   flow and gaseous exchange in chronic obstructive airway disease,
CC   or to treat malabsorptive syndromes in the intestinal tract.
CC   Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC   as an indicator of future metastatic risk. Antagonists can be used
CC   for treating e.g. conditions such as congestive heart failure,
CC   involving accumulations of fluid in the lung resulting from
CC   increases in vascular permeability.  The products can also be used
CC   for detection and diagnosis.
SQ   Sequence   1325 BP;    369 A;    335 C;    308 G;    313 T;


  Query Match             43.7%;  Score 874.8;  DB 1;  Length 1325;
  Best Local Similarity   84.2%;  Pred. No. 4.1e-248;
  Matches 1041;  Conservative    0;  Mismatches  172;  Indels   23;  Gaps    4;

Qy     323 ggagaatgccttttgaaacaattttctctagctgcctgatgtcaactgcttagtaatcag 382
           |||||||||||||| |||| |||||  ||||||||||    |||||||||||| ||| |
Db       1 GGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAGTCATCGG 60

Qy     383 tggata-ttgaaatattcaaaatgtacagagagtgggtagtggtgaatgttttcatgatg 441
           | || | || ||||||||||||||  |||| |||| | ||| |||| |  ||||||||
Db      61 TAGACATTTAAAATATTCAAAATGTATGGAGAATGGGGAATGGGGAATATCCTCATGATG 120

Qy     442 ttgtacgtccagctggtgcagggctccagtaatgaacatggaccagtga---------- 491
           ||  | ||  |  |||||||||||| ||| |  ||||||||||||||||
Db     121 TTCCATGTGTACTTGGTGCAGGGCTTCAGGAGCGAACATGGACCAGTGAAGGATTTTTCT 180

Qy     491 ----agcgatcatctcagtccacattggaacgatctgaacagcagatcagggctgcttct 546
               |||||||||| | |||||  |||||||||||||||||| |||||| | || ||||||
Db     181 TTTGAGCGATCATCCCGGTCCATGTTGGAACGATCTGAACAACAGATCCGAGCAGCTTCT 240

Qy     547 agtttggaggaactacttcgaattactcactctgaggactggaagctgtggagatgcagg 606
           ||||||||||  | || | |||  | ||||||||||||||||||||||||| ||||| ||
Db     241 AGTTTGGAGGAGTTGCTGCAAATCGCGCACTCTGAGGACTGGAAGCTGTGGCGATGCCGG 300
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Qy    607 ctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtccactagg 666
Db    301 TTGAAGCTCAAAAGTCTTGCCAGTATGGACTCACGCTCAGCATCCCATCGCTCCACCAGA 360

Qy    667 tttgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatggcaaaga 726
Db    361 TTTGCGGCAACTTTCTATGACACTGAAACACTAAAAGTTATAGATGAAGAATGGCAGAGG 420

Qy    727 actcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaagagtacc 786
Db    421 ACCCAATGCAGCCCTAGAGAGACATGCGTAGAAGTCGCCAGTGAGCTGGGGAAGACAACC 480

Qy    787 aacacattcttcaagcccccttgtgtgaacgtgttccgatgtggtggctgttgcaatgaa 846
Db    481 AACACATTCTTCAAGCCCCCCTGTGTAAATGTCTTCCGGTGTGGAGGCTGCTGCAACGAA 540

Qy    847 gagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttgagata 906
Db    541 GAGGGTGTGATGTGTATGAACACAAGCACCTCCTACATCTCCAAACAGCTCTTTGAGATA 600

Qy    907 tcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcatacaggt 966
Db    601 TCAGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTAAAATTGCCAACCATACGGGT 660

Qy    967 tgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatccatccag 1026
Db    661 TGTAAGTGCTTGCCCACGGGCCCCCGCCATCCTTACTCAATTATCAGAAGATCCATTCAG 720

Qy   1027 atccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatgctatgg 1086
Db    721 ACCCCAGAAGAAGATGAATGTCCTCATTCCAAGAAACTCTGTCCTATTGACATGCTGTGG 780

Qy   1087 gatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaacagaagac 1146
Db    781 GATAACACCAAATGTAAATGTGTTTTGCAAGACGAGACTCCACTGCCTGGGACAGAAGAC 840

Qy   1147 cactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaagatcgt 1206
Db    841 CACTCTTACCTCCAGGAACCCACTCTCTGTGGACCGCACATGACGTTTGATGAAGATCGC 900

Qy   1207 tgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaaaactgc 1266
Db    901 TGTGAGTGCGTCTGTAAAGCACCATGTCCGGGAGATCTCATTCAGCACCCGGAAAACTGC 960

Qy   1267 agttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagctatttcac 1326
Db    961 AGTTGCTTTGAGTGCAAAGAAAGTCTGGAGAGCTGCTGCCAAAAGCACAAGATTTTTCAC 1020

Qy   1327 ccagacacctgcagctgtgaggacagatgccccttttcataccagaccatgtgcaagtggc 1386
Db   1021 CCAGACACCTGCAGCTGTGAGGACAGATGTCCTTTTCACACCAGAACATGTGCAAGTAGA 1080

Qy   1387 aaaacagcatgtgcaaagcattgccgctttccaaaggagaaaagggctgcccaggggccc 1446
Db   1081 AAGCCAGCCTGTGGAAAGCACTGGCGCTTTCCAAAGGAGACAAGG---GCCCAGGGACTC 1137

Qy   1447 cacagccgaaagaatccttgattca----gcgttccaagttccccatccctgtcatttttt 1502
Db   1138 TACAGCCAGGAGAACCCTTGATTCAACTTCCTTTCAAGTCCCCCCATCTCTGTCATTTTA 1197

Qy   1503 aacagcatgctgctttgccaagttgctgtcactgtt 1538
Db   1198 AACAGCTCACTGCTTTGTCAAGTTGCTGTCACTGTT 1233


RESULT   9
V15178
ID   V15178 standard; cDNA to mRNA; 1491 BP.
AC   V15178;
DT   22-JUN-1998  (first entry)
DE   Rat vascular endothelial growth factor D encoding cDNA.
KW   Rate; vascular endothelial growth factor D; VEGF-D; gene therapy;
KW   inflammation; oedema; ds.
OS   Rattus sp.
FH   Key             Location/Qualifiers
FT   CDS             270. .1250
FT                   /*tag= a
FT                   /product= "VEGF-D"
PN   WO9802543-A1.
PD   22-JAN-1998.
PF   15-JUL-1997; J02456.
PR   15-JUL-1996; JP-185216.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PI   Hirata Y, Nezu J;
DR   WPI; 98-110591/10.
DR   P-PSDB; W44296.
PT   VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT   treating oedema
PS   Example 8; Page 35-38; 52pp; Japanese.
CC   The present sequence encodes rat vascular endothelial growth factor D
CC   (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC   the protein, may be useful in, e.g. gene therapy and in treatment of
CC   inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
CC   DNA sequences may be used for screening for the compounds which bind to
CC   the VEGF-D protein.
SQ   Sequence   1491 BP;    399 A;    336 C;    339 G;    417 T;


  Query Match             40.2%;  Score 806.6;  DB 1;  Length 1491;
  Best Local Similarity   81.6%;  Pred. No. 5.8e-228;
  Matches 1004;  Conservative    0;  Mismatches  199;  Indels   28;  Gaps    5;

Qy    148 ccaccttctgattatttttggag-----aacattttgatttttttcatctctctctcccc 202
Db      2 CCACCTCTTGATTATTTGTGCAGCGGGAAACTTTGAAATAGTTTTCATCTCTTTCTCCCA 61

Qy    203 acccctaagattgtgcaaaaaaagcgta--ccttgcctaattgaaataatttcattggat 260
Db     62 TACTAAGATTGTGTGTGGCCGTGGGGGAGTCCTTGACTAACTCAAGTCATTTCATTGGAT 121

Qy    261 tttgatcagaactgatcatttgg-----ttttctgtgtgaagttttgaggtttcaaactt 315
Db    122 TTTGATTACAACTGATCATGTGATATTTTTTTCCATGTAAAGTTTTGGGGCTTCAAACTT 181

Qy    316 tccttctggagaatgccttttgaaacaattttctctagctgcctgatgtcaactgcttag 375
Db    182 TGCTTCTGGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAG 241

Qy    376 taatcagtggata-ttgaaatattcaaaatgtacagagagtgggtagtggtgaatgtttt 434
Db    242 CCATCAGTGGACATTTGAAATATTCAAAATGTATGGAGAGTGGGCCGCAGTGAATATTCT 301

Qy    435 catgatgttgtacgtccagctggtgcagggctccagtaatgaacatggaccagtga---- 491
Db    302 CATGATGTCCTATGTGTACCTGGTGCAGGGCTTCAGTATTGAACACCGAGCAGTGAAGGA 361

Qy    491 -----------agcgatcatctcagtccacattggaacgatctgaacagcagatcagggc 539
Db    362 TGTTTCTCTTGAGCGATCATCCCGGTCTGTGTTGGAACGTTCTGAACAACAGATCCGCGC 421

Qy    540 tgcttctagtttggaggaactacttcgaattactcactctgaggactggaagctgtggag 599
Db    422 GGCTTCTACTTTGGAAGAGTTGCTGCAAGTCGCACACTCTGAGGACTGGAAGCTGTGGCG 481

Qy    600 atgcaggctgaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtc 659
Db    482 GTGCCGGTTGAAGCTTAAAAGTCTTGCCAATGTGGACTCGCGCTCAACATCCCATCGCTC 541

Qy    660 cactaggtttgcggcaacttttctatgacattgaaacactaaaagttatagatgaagaatg 719
Db    542 CACCAGATTTGCGGCAACTTTCTATGATACTGAAACACTAAAAGTTATAGATGAAGAATG 601

Qy    720 gcaaagaactcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaa 779
Db    602 GCAGAGGACCCAATGCAGCCCTAGAGAGACATGCGTAGAAGTCGCCAGTGAGCTGGGGAA 661
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Qy    780 gagtaccaacacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttg 839
          ||  |||||||||||| |||||||||||||||||| || || ||||| ||||| || || ||
Db    662 GACAACCAACACATTTTTCAAGCCCCCTTGTGTAAATGTCTTCCGGTGTGGAGGATGCTG 721

Qy    840 caatgaagagagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctt 899
          |||||||||||||  | || |||||||||| |||||||| ||||| ||||||||||||||
Db    722 CAATGAAGAGAGCGTGATGTGTATGAACACAAGCACCTCCTACATCTCCAAACAGCTCTT 781

Qy    900 tgagatatcagtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatca 959
          ||||||||||||||| |||||||||| || || ||||||||||||||| ||||||| ||
Db    782 TGAGATATCAGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTAAAATTGCCAACCA 841

Qy    960 tacaggttgtaagtgcttgccaacagccccccgccatccatactcaattatcagaagatc 1019
          ||| |||||||||| ||||| || | |||||| ||||| || ||||||||||||||||||
Db    842 TACGGGTTGTAAGTGTTTGCCCACGGGCCCCCGGCATCCTTATTCAATTATCAGAAGATC 901

Qy   1020 catccagatccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacat 1079
          ||| ||||||||  |||||||||||  ||| | |||||||||||||||||||| |||||||
Db    902 CATTCAGATCCCAGAAGAAGATCAATGTCCTCATTCCAAGAAACTCTGTCCTGTTGACAT 961

Qy   1080 gctatgggatagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaac 1139
          ||| ||||||| || |||||||||||||||||| || || || ||||||||  |||| ||
Db    962 GCTGTGGGATAACACCAAATGTAAATGTGTTTTACAAGATGAGAATCCACTGCCTGGGAC 1021

Qy   1140 agaagaccactctcatctccaggaaccagctctctgtgggccacacatgatgtttgacga 1199
          |||||||||||| | |||||||||| |||||||||| ||||||||||||||||||| ||
Db   1022 AGAAGACCACTCTTACCTCCAGGAACCCGCTCTCTGTGGACCACACATGATGTTTGATGA 1081

Qy   1200 agatcgttgcgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaa 1259
          ||||||  |||||||||||||||||| ||||||||||   |||||| || ||||||||  |
Db   1082 AGATCGCTGCGAGTGTGTCTGTAAAGCACCATGTCCTGGAGATCTCATTCAGCACCCGGA 1141

Qy   1260 aaactgcagttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagct 1319
          |||||||||||||||||| |||||||||||||||| | ||| ||||| ||||||||| |
Db   1142 AAACTGCAGTTGCTTTGAATGCAAAGAAAGTCTGGAAAGCTGTTGCCAAAAGCACAAGAT 1201

Qy   1320 atttcacccagacacctgcagctgtgaggac 1350
            |||||||| |||||||||| |    || |
Db   1202 GTTTCACCCTGACACCTGCAGATCAATGGTC 1232
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RESULT  10
V20809
ID   V20809 standard; cDNA; 1135 BP.
AC   V20809;
DT   03-AUG-1998  (first entry)
DE   Mus musculus vascular endothelial growth factor D2 (VEGF-D2) gene.
KW   vascular endothelial growth factor; VEGF-D; angiogenesis;
KW   modification; acceleration; wound healing; tissue; organ;
KW   transplants; collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW   detection; diagnosis; congestive heart failure; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             95. .1060
FT                   /*tag=  a
FT                   /product= VEGF-D2
FT                   /note= "isolated from lung tissue"
PN   WO9807832-A1.
PD   26-FEB-1998.
PF   21-AUG-1997; U14696.
PR   01-JUL-1997; US-051426.
PR   23-AUG-1996; AU-001825.
PR   23-AUG-1996; US-023751.
PR   11-NOV-1996; AU-003554.
PR   14-NOV-1996; US-031097.
PR   05-FEB-1997; AU-004954.
PR   10-FEB-1997; US-038814.
PR   19-JUN-1997; AU-007435.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR   WPI; 98-179057/16.
DR   P-PSDB; W53243.
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung,
PT   heart or intestinal disorders
PS   Claim 6; Pages 62-63; 101pp; English.
CC   The sequence is that encoding mouse vascular endothelial growth factor
CC   D2 (VEGF-D2). VEGF-D2 can be used for e.g. acceleration of angiogenesis
CC   in wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis,
CC   such as coronary artery disease, and inhibition of angiogenesis in
CC   the treatment of cancer or of diabetic retinopathy.  It can also be
CC   used in the treatment of lung disorders to improve blood circulation
CC   in the lung and/or gaseous exchange between the lungs and the blood
CC   stream or to improve blood circulation to the heart and O2 gas
CC   permeability in cases of cardiac insufficiency, to improve blood
CC   flow and gaseous exchange in chronic obstructive airway disease,
CC   or to treat malabsorptive syndromes in the intestinal tract.
CC   Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC   as an indicator of future metastatic risk. Antagonists can be used
CC   for treating e.g. conditions such as congestive heart failure,
CC   involving accumulations of fluid in the lung resulting from
CC   increases in vascular permeability.  The products can also be used
CC   for detection and diagnosis.
SQ   Sequence   1135 BP;    310 A;    278 C;    266 G;    281 T;
```

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  Query Match             39.7%;  Score 796.4;  DB 1;  Length 1135;
  Best Local Similarity   85.9%;  Pred. No. 5e-225;
  Matches  895;  Conservative    0;  Mismatches  146;  Indels    1;  Gaps    1;

Qy    310 aaactttccttctggagaatgccttttgaaacaattttctctagctgcctgatgtcaact 369
          |||||||  |||||||||||||||||||| |||| |||||  ||||||||||    |||||
Db      1 AAACTTTGCTTCTGGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACAACT 60

Qy    370 gcttagtaatcagtggata-ttgaaatattcaaaatgtacagagagtgggtagtggtgaa 428
          |||||||  ||| || || | || ||||||||||||||||  |||| |||| | ||| |||
Db     61 GCTTAGTCATCGGTAGACATTTAAAATATTCAAAATGTATGGAGAATGGGGAATGGGGAA 120

Qy    429 tgttttcatgatgttgtacgtccagctggtgcagggctccagtaatgaacatggaccagt 488
          | |  ||||||||||  | ||  |  |||||||||||| ||| |  ||||||||||||
Db    121 TATCCTCATGATGTTCCATGTGTACTTGGTGCAGGGCTTCAGGAGCGAACATGGACCAGT 180

Qy    489 gaagcgatcatctcagtccacattggaacgatctgaacagcagatcagggctgcttctag 548
          |||||||||||| | |||||  ||||||||||||||||| |||||| | || ||||||||
Db    181 GAAGCGATCATCCCGGTCCATGTTGGAACGATCTGAACAACAGATCCGAGCAGCTTCTAG 240

Qy    549 tttggaggaactacttcgaattactcactctgaggactggaagctgtggagatgcaggct 608
          |||||||||  | || | |||  | |||||||||||||||||||||||| ||||| || |
Db    241 TTTGGAGGAGTTGCTGCAAATCGCGCACTCTGAGGACTGGAAGCTGTGGCGATGCCGGTT 300

Qy    609 gaggctcaaaagttttaccagtatggactctcgctcagcatcccatcggtccactaggtt 668
          || |||||||||| || |||||||||||| |||||||||||||||| ||||| || ||
Db    301 GAAGCTCAAAAGTCTTGCCAGTATGGACTCACGCTCAGCATCCCATCGCTCCACCAGATT 360

Qy    669 tgcggcaactttctatgacattgaaacactaaaagttatagatgaagaatggcaaagaac 728
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||| || ||
Db    361 TGCGGCAACTTTCTATGACACTGAAACACTAAAAGTTATAGATGAAGAATGGCAGAGGAC 420

Qy    729 tcagtgcagccctagagaaacgtgcgtggaggtggccagtgagctggggaagagtaccaa 788
           || |||||||||||||| || ||||| || || ||||||||||||||||||  |||||
Db    421 CCAATGCAGCCCTAGAGAGACATGCGTAGAAGTCGCCAGTGAGCTGGGGAAGACAACCAA 480

Qy    789 cacattcttcaagccccccttgtgtgaacgtgttccgatgtggtggctgttgcaatgaaga 848
          |||||||||||||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Db    481 CACATTCTTCAAGCCCCCCTGTGTAAATGTCTTCCGGTGTGGAGGCTGCTGCAACGAAGA 540

Qy    849 gagccttatctgtatgaacaccagcacctcgtacatttccaaacagctctttgagatatc 908
          | |  | || |||||||||||| |||||||| ||||| ||||||||||||||||||||||
Db    541 GGGTGTGATGTGTATGAACACAAGCACCTCCTACATCTCCAAACAGCTCTTTGAGATATC 600
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Qy     909 agtgcctttgacatcagtacctgaattagtgcctgttaaagttgccaatcatacaggttg 968
           ||||||| |||||||||| || || ||||||||||||||| ||||||| ||||| |||||
Db     601 AGTGCCTCTGACATCAGTGCCCGAGTTAGTGCCTGTTAAAATTGCCAACCATACGGGTTG 660

Qy     969 taagtgcttgccaacagccccccgccatccatactcaattatcagaagatccatccagat 1028
           |||||||||||| || | |||||||||||| ||||||||||||||||||||| ||||
Db     661 TAAGTGCTTGCCCACGGGCCCCCGCCATCCTTACTCAATTATCAGAAGATCCATTCAGAC 720

Qy    1029 ccctgaagaagatcgctgttcccattccaagaaactctgtcctattgacatgctatggga 1088
           ||| |||||||||   ||| | ||||||||||||||||||||||||||||||| |||||
Db     721 CCCAGAAGAAGATGAATGTCCTCATTCCAAGAAACTCTGTCCTATTGACATGCTGTGGGA 780

Qy    1089 tagcaacaaatgtaaatgtgttttgcaggaggaaaatccacttgctggaacagaagacca 1148
           || || |||||||||||||||||||| || || | |||||  |||| ||||||||||
Db     781 TAACACCAAATGTAAATGTGTTTTGCAAGACGAGACTCCACTGCCTGGGACAGAAGACCA 840

Qy    1149 ctctcatctccaggaaccagctctctgtgggccacacatgatgtttgacgaagatcgttg 1208
           |||| | ||||||||||  |||||||||| || |||||| |||||| |||||||| ||
Db     841 CTCTTACCTCCAGGAACCCACTCTCTGTGGACCGCACATGACGTTTGATGAAGATCGCTG 900

Qy    1209 cgagtgtgtctgtaaaacaccatgtcccaaagatctaatccagcaccccaaaaactgcag 1268
            ||||| |||||||||| ||||||||||   |||||| || ||||||||  ||||||||||
Db     901 TGAGTGCGTCTGTAAAGCACCATGTCCGGGAGATCTCATTCAGCACCCGGAAAACTGCAG 960

Qy    1269 ttgctttgagtgcaaagaaagtctggagacctgctgccagaagcacaagctatttcaccc 1328
           |||||||||||||||||||||||||| |||||||| |||||||| | ||||||||
Db     961 TTGCTTTGAGTGCAAAGAAAGTCTGGAGAGCTGCTGCCAAAAGCACAAGATTTTTCACCC 1020

Qy    1329 agacacctgcagctgtgaggac 1350
           |||||||||||| |    || |
Db    1021 AGACACCTGCAGGTCAATGGTC 1042


RESULT  11
T84277
ID   T84277 standard; cDNA; 1836 BP.
AC   T84277;
DT   10-NOV-1997  (first entry)
DE   Mouse Flt4 receptor tyrosine kinase ligand VEGF-C cDNA.
KW   VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; mouse;
KW   vascular endothelial growth factor receptor-3; ligand;
KW   angiogenesis; wound healing; lymph vessel; therapy; diagnosis; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   cds             168. .1415
FT                   /*tag= a
PN   WO9705250-A2.
PD   13-FEB-1997.
PF   01-AUG-1996; FI0427.
PR   28-JUN-1996; US-671573.
PR   01-AUG-1995; US-510133.
PR   12-JAN-1996; US-585895.
PR   14-FEB-1996; US-601132.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI   Alitalo K,  Joukov V;
DR   WPI; 97-145688/13.
DR   P-PSDB; W00933.
PT   Flt4 receptor tyrosine kinase ligand and related nucleic acid - used
PT   to modulate growth of endothelial cells and for diagnosis of
PT   endothelial cell diseases
PS   Example 20; Page 119-121; 183pp; English.
CC   This cDNA clone codes for mouse VEGF-C (W00933), a novel ligand
CC   that binds specifically to the Flt4 receptor tyrosine kinase
CC   (VEGFR-3), stimulating phosphorylation of the receptor.  The clone
CC   was isolated from a 12-day mouse embryonal cDNA library using a
CC   fragment of human VEGF-C cDNA (see also T84276) as probe.  The
CC   isolated polynucleotide can be used to produce recombinant
CC   polypeptides corresponding to non-human mammalian variants of
CC   VEGF-C.  The mouse VEGF-C gene contains 6 introns (see T84315-26).
SQ   Sequence   1836 BP;    521 A;    431 C;    451 G;    433 T;
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  Query Match             6.9%;  Score 137.6;  DB 1;  Length 1836;
  Best Local Similarity   52.7%;  Pred. No. 1.4e-30;
  Matches  374;  Conservative    0;  Mismatches  324;  Indels   12;  Gaps    3;

Qy     523 gaacagcagatcagggctgcttctagtttggaggaactacttcgaattactcactctgag 582
           ||  ||||| |  || ||| || ||  | || || ||  |     |     || | ||
Db     336 GAGGAGCAGTTGCGGTCTGTGTCCAGCGTAGATGAGCTGATGTCTGTCCTGTACCCAGAC 395

Qy     583 gactggaagctgtggagatgcaggctgaggctcaaaagttttaccagtatggactctcgc 642
           |||||||  |||  |  |||  |||| ||        | |             |
Db     396 TACTGGAAAATGTACAAGTGCCAGCTGCGGAAAGGCGGCTGGCAGCAGCCCACCCTCAAT 455

Qy     643 tcagcatcccatcggtccactaggtttgcggcaactttctatgacattgaaacactaaaa 702
           |     |              |  ||||| ||  |    ||| |||  || |  || |||
Db     456 ACCAGGACAGGGGACAGTGTAAAATTTGCTGCTGCACATTATAACACAGAGATCCTGAAA 515

Qy     703 gttatagatgaagaatggcaaagaactcagtgcagccctagagaaacgtgcgtggaggtg 762
             ||| ||| | || |||  ||  ||||| |||| ||  | ||   |||  | || |||
Db     516 AGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGTGAGGTGTGTATAGATGTG 575

Qy     763 gccagtgagctggggaagagtaccaacacattcttcaagccccttgtgtgaacgtgttc 822
           |  |  ||| | ||        || ||||| ||||| || || || ||||||  ||| | |
Db     576 GGGAAGGAGTTTGGAGCAGCCACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTAC 635

Qy     823 cgatgtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcgtac 882
           |||||||  || || |||||    ||| | ||    || ||||||||||||||    |||
Db     636 AGATGTGGGGGTTGCTGCAACAGGGAGGGGCTGCAGTGCATGAACACCAGCACAGGTTAC 695

Qy     883 atttccaaacagctctttgagatatcagtgcctttgacatcagtacctgaattagtgcct 942
           |   |||   | | |||||  ||  |||||||| |  ||  ||  ||  ||  |||  |
Db     696 CTCAGCAAGACGTTGTTTGAAATTACAGTGCCTCTCTCACAAGGCCCCAAACCAGTCACA 755

Qy     943 gttaaagttgccaatcatacaggttgtaagtgcttgccaaca------gccccccgccat 996
           | |   ||||||||||  ||    ||   |||| || | | |       |    | | ||
Db     756 ATCAGTTTTGCCAATCACACTTCCTGCCGGTGCATGTCTAAACTGGATGTTTACAGACAA 815

Qy     997 ccatactcaattatcagaagatccatccagatccctgaagaagatcgctgttcccattcc 1056
             | |||||||| ||| | ||  | |       |   |  | |  |     |   |  |
Db     816 GTTCATTCAATTATTAGACGTTCTCTGCCAGCAACATTACCACAGTGTCAGGCAGCTAAC 875

Qy    1057 aagaaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgtgttttgcag 1116
           |||| |   ||||| |   ||    | ||| ||| | ||| ||   ||   |    |||
Db     876 AAGACA---TGTCCAACAAACTATGTGTGGAATAACTACATGTGCCGATGCCTGGCTCAG 932

Qy    1117 gaggaaaatccacttgctggaa---cagaagaccactctcatctccaggaaccagctctc 1173
           ||||   |    ||  |  ||     |||||  ||||                |  | ||
Db     933 CAGGATTTTATCTTTTATTCAAATGTTGAAGATGACTCAACCAATGGATTCCATGATGTC 992

Qy    1174 tgtgggccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaa 1223
           ||||| ||  ||| |  | | || |||||    ||  |||||||||| ||
Db     993 TGTGGACCCAACAAGGAGCTGGATGAAGACACCTGTCAGTGTGTCTGCAA 1042


RESULT  12
V52577
ID   V52577 standard; cDNA; 1836 BP.
AC   V52577;
DT   14-DEC-1998  (first entry)
DE   Mouse vascular endothelial growth factor C gene.
KW   Flt4; vascular endothelial growth factor C; vascular endothelial cell;
KW   lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation;
KW   lymphangiogenesis; oedema; elephantiasis; Milroy's disease; ss.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   CDS             168. .1415
FT                   /*tag= a
FT                   /product= "VEGF-C"
PN   WO9833917-A1.
PD   06-AUG-1998.
PF   02-FEB-1998; U01973.
PR   05-FEB-1997; US-795430.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
```

PI Alitalo K, Joukov V;
DR WPI; 98-437470/37.
DR P-PSDB; W75742.
PT New isolated vascular endothelial growth factor polypeptide(s) -
PT used to develop products for treating, e.g. cancers, inflammation,
PT oedema, granulocytopenia or for wound healing or tissue
PT transplantation
PS Example 20; Page 117-119; 177pp; English.
CC The vascular endothelial growth factor C (VEGF-C) polypeptides have
CC activities affecting growth and migration of vascular endothelial cells,
CC promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC increasing vascular permeability, and affecting myelopoiesis. The
CC products can be used for stimulating angiogeneses, for inhibiting
CC angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC They can also be used for modulating the growth of endothelial cells.
CC They can also be used to stimulate lymphocyte production and maturation,
CC and to promote or inhibit trafficking of leucocytes between tissues and
CC lymphatic vessels or to affect migration in and out of the thymus.
SQ Sequence 1836 BP; 521 A; 432 C; 450 G; 433 T;

Query Match 6.9%; Score 137.6; DB 1; Length 1836;
Best Local Similarity 52.7%; Pred. No. 1.4e-30;
Matches 374; Conservative 0; Mismatches 324; Indels 12; Gaps 3;

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Qy    523 gaacagcagatcagggctgcttctagtttggaggaaactacttcgaattactcactctgag 582
          ||  ||||| |  || ||| || || |  | || || ||  |      |     || | ||
Db    336 GAGGAGCAGTTGCGGTCTGTGTCCAGCGTAGATGAGCTGATGTCTGTCCTGTACCCAGAC 395

Qy    583 gactggaagctgtggagatgcaggctgaggctcaaaagttttaccagtatggactctcgc 642
          |||||||  |||  |  |||  |||| ||       | |                |
Db    396 TACTGGAAAATGTACAAGTGCCAGCTGCGGAAAGGCGGCTGGCAGCAGCCCACCCTCAAT 455

Qy    643 tcagcatcccatcggtccactaggtttgcggcaactttctatgacattgaaacactaaaa 702
          |    |             |  ||||| ||  |    ||| |||  || |  || |||
Db    456 ACCAGGACAGGGGACAGTGTAAAATTTGCTGCTGCACATTATAACACAGAGATCCTGAAA 515

Qy    703 gttatagatgaagaatggcaaagaactcagtgcagccctagagaaacgtgcgtggaggtg 762
          ||| ||| | || |||  ||  ||||| ||||  ||  | ||   |||  | || |||
Db    516 AGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGTGAGGTGTGTATAGATGTG 575

Qy    763 gccagtgagctggggaagagtaccaacacattcttcaagccccctgtgtgaacgtgttc 822
          |  |  ||| | ||        || ||||| ||||| || || || ||||||  ||| | |
Db    576 GGGAAGGAGTTTGGAGCAGCCACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTAC 635

Qy    823 cgatgtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcgtac 882
          |||||||  || || |||||    ||| | ||    || ||||||||||||||    |||
Db    636 AGATGTGGGGGTTGCTGCAACAGCGAGGGGCTGCAGTGCATGAACACCAGCACAGGTTAC 695

Qy    883 atttccaaacagctctttgagatatcagtgcctttgacatcagtacctgaattagtgcct 942
          |   |||   | | ||||| ||  |||||||| |  ||  ||  ||  ||  |||  |
Db    696 CTCAGCAAGACGTTGTTTGAAATTACAGTGCCTCTCTCACAAGGCCCCAAACCAGTCACA 755

Qy    943 gttaaagttgccaatcatacaggttgtaagtgcttgccaaca------gccccccgccat 996
          | |  ||||||||||  ||    ||   |||| || | | |      |    | | ||
Db    756 ATCAGTTTTGCCAATCACACTTCCTGCCGGTGCATGTCTAAACTGGATGTTTACAGACAA 815

Qy    997 ccatactcaattatcagaagatccatccagatccctgaagaagatcgctgttcccattcc 1056
            | |||||||| ||| | ||  | |       |   |  | |  |      |   |  |
Db    816 GTTCATTCAATTATTAGACGTTCTCTGCCAGCAACATTACCACAGTGTCAGGCAGCTAAC 875

Qy   1057 aagaaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgtgttttgcag 1116
          ||||  |   ||||| |   ||    | ||| ||| | |||  ||   |||  |    |||
Db    876 AAGACA---TGTCCAACAAACTATGTGTGGAATAACTACATGTGCCGATGCCTGGCTCAG 932

Qy   1117 gaggaaaatccacttgctggaa---cagaagaccactctcatctccaggaaccagctctc 1173
          ||||   |    ||  |  ||     |||||  ||||                |  | | ||
Db    933 CAGGATTTTATCTTTTATTCAAATGTTGAAGATGACTCAACCAATGGATTCCATGATGTC 992

Qy   1174 tgtgggccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaa 1223
          |||||  ||  ||| |  | | ||  |||||    ||  |||||||||| ||
```

Db 993 TGTGGACCCAACAAGGAGCTGGATGAAGACACCTGTCAGTGTGTCTGCAA 1042

RESULT 13
T84300
ID T84300 standard; cDNA; 1741 BP.
AC T84300;
DT 10-NOV-1997 (first entry)
DE Quail Flt4 receptor tyrosine kinase ligand VEGF-C cDNA.
KW VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; quail;
KW vascular endothelial growth factor receptor-3; ligand;
KW angiogenesis; wound healing; lymph vessel; therapy; diagnosis; ss.
OS Coturnix coturnix.
FH Key Location/Qualifiers
FT cds 453. .1709
FT /*tag= a
PN WO9705250-A2.
PD 13-FEB-1997.
PF 01-AUG-1996; FI0427.
PR 28-JUN-1996; US-671573.
PR 01-AUG-1995; US-510133.
PR 12-JAN-1996; US-585895.
PR 14-FEB-1996; US-601132.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alitalo K, Joukov V;
DR WPI; 97-145688/13.
DR P-PSDB; W00934.
PT Flt4 receptor tyrosine kinase ligand and related nucleic acid - used
PT to modulate growth of endothelial cells and for diagnosis of
PT endothelial cell diseases
PS Example 20; Page 124-126; 183pp; English.
CC This cDNA clone codes for quail VEGF-C (W00934), a novel ligand
CC that binds specifically to the Flt4 receptor tyrosine kinase
CC (VEGFR-3), stimulating phosphorylation of the receptor. The clone
CC was isolated from a quail cDNA library using mouse (see T84277)
CC and human (see T84276) VEGF-C cDNA fragments as probes. The
CC isolated polynucleotide can be used to produce recombinant
CC polypeptides corresponding to non-human mammalian variants of
CC VEGF-C.
SQ Sequence 1741 BP; 445 A; 455 C; 449 G; 392 T;

Query Match 6.7%; Score 134; DB 1; Length 1741;
Best Local Similarity 52.4%; Pred. No. 1.6e-29;
Matches 377; Conservative 0; Mismatches 325; Indels 18; Gaps 3;

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Qy    523 gaacagcagatcagggctgcttctagtttggaggaaactacttcgaattactcactctgag 582
          ||| ||||| |  |  |||  || ||| |||| |||||  |   | |   | || | ||
Db    618 GAAGAGCAGTTGCGATCTGTGTCCAGTGTGGATGAACTCATGACAGTACTTTACCCAGAA 677

Qy    583 gactggaagctgtggagatgcaggctgaggctcaaaagttttaccagta---------- 632
          |||||||  |||  | |||   | |||||     | |||        |
Db    678 TACTGGAAAATGTTCAAATGTCAGTTGAGGAAAGGAGGTTGGCAACACAACAGGGAACAC 737

Qy    632 -tggactctcgctcagcatcccatcggtccactaggtttgcggcaactttctatgacatt 690
           ||||   ||  |||  ||   ||    |  ||||| ||| |    ||| |
Db    738 TCCAGCTCTGATACAAGATCAGATGATTCATTGAAATTTGCCGCAGCACATTATAATGCA 797

Qy    691 gaaacactaaaagttatagatgaagaatggcaaagaactcagtgcagccctagagaaacg 750
          || |  || |||  ||| ||| ||||||  || ||| ||| |||  ||  | |||  |
Db    798 GAGATCCTGAAAAGTATTGATACTGAATGGAGAAAAACCCAGGGCATGCCACGTGAAGTG 857

Qy    751 tgcgtggaggtggccagtgagctggggaagagtaccaacacattcttcaagccccccttgt 810
          || ||||| |||  |  ||| | ||    | ||| ||||| ||||| || ||||| |||
Db    858 TGTGTGGATTTGGGGAAAGAGTTTGGAGCAACTACAAACACCTTCTTTAAACCCCCGTGT 917

Qy    811 gtgaacgtgttccgatgtggtggctgttgcaatgaagagagccttatctgtatgaacacc 870
          ||   | | | | ||||||| || || ||||||   ||  | ||    |||||||| | |
Db    918 GTATCCATCTACAGATGTGGAGGTTGCTGCAATAGTGAAGGACTCCAGTGTATGAATATC 977

Qy    871 agcacctcgtacatttccaaacagctctttgagatatcagtgcctttgacatcagtacct 930
          |||||    |||||  |||      | ||||||||  ||||||||  |  |    |  ||
Db    978 AGCACAAATTACATCAGCAAGACATTGTTTGAGATTACAGTGCCTCTCTCTCATGGCCCC 1037
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Qy     931 gaattagtgcctgttaaagttgccaatcatacaggttgtaagtgcttgccaaca---gcc 987
           ||   ||  | || |   |||||||||| ||    ||    ||| || | |     |
Db    1038 AAACCTGTAACAGTCAGTTTTGCCAATCACACGTCCTGCCGATGCATGTCTAAGTTGGAT 1097

Qy     988 ccccgccatccatactcaattatcagaagatccatccagatccctgaagaagatcgctgt 1047
             |   | |        ||||| ||||     |  |     |  | ||  ||  |||
Db    1098 GTTTACAGACAAGTTCATTCTATCATAAGACGTTCCTTGCCAGCAACACAAACTCAGTGT 1157

Qy    1048 tcccattccaagaaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgt 1107
             | || ||   |||||| |   |     | ||| |||   | |  || | |||
Db    1158 CATGTGGCAAACAAGACCTGTCCAAAAAATCATGTCTGGAATAATCAGATTTGCAGATGC 1217

Qy    1108 gttttgcaggaggaaaatccacttgctggaacagaagaccactctcatctccaggaacca 1167
           |    ||| | ||   |    |  ||          |   | ||| |       |||  |
Db    1218 TTAGCACAGCACGATTTTGGTTTCTCTTCTCACCTTGGAGATTCTGACACATCTGAAGGA 1277

Qy    1168 ---gctctctgtgggccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaaa 1224
              | | ||||||||  |||    | | || |||||    ||  | || |||||  |||
Db    1278 TTCCATATTTGTGGGCCCAACAAAGAGCTGGATGAAGAAACCTGTCAATGCGTCTGCAAA 1337
```

RESULT 14
V52578
ID V52578 standard; cDNA; 1741 BP.
AC V52578;
DT 14-DEC-1998 (first entry)
DE Quail vascular endothelial growth factor C gene.
KW Flt4; vascular endothelial growth factor C; vascular endothelial cell;
KW lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation;
KW lymphangiogenesis; oedema; elephantiasis; Milroy's disease; ss.
OS Coturnix sp.

FH	Key	Location/Qualifiers
FT	CDS	453. .1709
FT		/*tag= a
FT		/product= "VEGF-C"

PN WO9833917-A1.
PD 06-AUG-1998.
PF 02-FEB-1998; U01973.
PR 05-FEB-1997; US-795430.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
PI Alitalo K, Joukov V;
DR WPI; 98-437470/37.
DR P-PSDB; W75743.
PT New isolated vascular endothelial growth factor polypeptide(s) -
PT used to develop products for treating, e.g. cancers, inflammation,
PT oedema, granulocytopenia or for wound healing or tissue
PT transplantation
PS Example 20; Page 121-123; 177pp; English.
CC The vascular endothelial growth factor C (VEGF-C) polypeptides have
CC activities affecting growth and migration of vascular endothelial cells,
CC promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC increasing vascular permeability, and affecting myelopoiesis. The
CC products can be used for stimulating angiogeneses, for inhibiting
CC angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC They can also be used for modulating the growth of endothelial cells.
CC They can also be used to stimulate lymphocyte production and maturation,
CC and to promote or inhibit trafficking of leucocytes between tissues and
CC lymphatic vessels or to affect migration in and out of the thymus.
SQ Sequence 1741 BP; 445 A; 455 C; 449 G; 392 T;

Query Match 6.7%; Score 134; DB 1; Length 1741;
Best Local Similarity 52.4%; Pred. No. 1.6e-29;
Matches 377; Conservative 0; Mismatches 325; Indels 18; Gaps 3;

```
Qy     523 gaacagcagatcagggctgcttctagtttggaggaactacttcgaattactcactctgag 582
           ||| ||||| |  |  |||  || ||| |||| |||||  |   | |   | || | ||
Db     618 GAAGAGCAGTTGCGATCTGTGTCCAGTGTGGATGAACTCATGACAGTACTTTACCCAGAA 677

Qy     583 gactggaagctgtggagatgcaggctgaggctcaaaagttttaccagta---------- 632
           |||||||  |||  | |||   | |||||     | |||         |
Db     678 TACTGGAAAATGTTCAAATGTCAGTTGAGGAAAGGAGGTTGGCAACACAACAGGGAACAC 737

Qy     632 -tggactctcgctcagcatcccatcggtccactaggtttgcggcaactttctatgacatt 690
            ||||    ||  |||  ||   ||     |  ||||| ||| |    ||| |
Db     738 TCCAGCTCTGATACAAGATCAGATGATTCATTGAAATTTGCCGCAGCACATTATAATGCA 797

Qy     691 gaaaacactaaaagttatagatgaagaatggcaaagaactcagtgcagccctagagaaacg 750
           || |  || |||  ||| |||   ||||||  || ||| ||| |||  ||  | |||  |
Db     798 GAGATCCTGAAAAGTATTGATACTGAATGGAGAAAAACCCAGGGCATGCCACGTGAAGTG 857

Qy     751 tgcgtggaggtggccagtgagctggggaagagtaccaacacattcttcaagccccttgt 810
           || |||||  |||  |  ||| | ||    | ||| ||||| ||||| || ||||| |||
Db     858 TGTGTGGATTTGGGGAAAGAGTTTGGAGCAACTACAAACACCTTCTTTAAACCCCCGTGT 917

Qy     811 gtgaacgtgttccgatgtggtggctgttgcaatgaagagagccttatctgtatgaacacc 870
           ||   | | | | |||||||  || || ||||||   ||  | ||    |||||||| | |
Db     918 GTATCCATCTACAGATGTGGAGGTTGCTGCAATAGTGAAGGACTCCAGTGTATGAATATC 977

Qy     871 agcacctcgtacatttccaaacagctctttgagatatcagtgcctttgacatcagtacct 930
           |||||    |||||   |||     | ||||||||  ||||||||  |  |    |  ||
Db     978 AGCACAAATTACATCAGCAAGACATTGTTTGAGATTACAGTGCCTCTCTCTCATGGCCCC 1037

Qy     931 gaattagtgcctgttaaagttgccaatcatacaggttgtaagtgcttgccaaca---gcc 987
           ||   ||  | || |   |||||||||| ||    ||    ||| || | |     |
Db    1038 AAACCTGTAACAGTCAGTTTTGCCAATCACACGTCCTGCCGATGCATGTCTAAGTTGGAT 1097

Qy     988 ccccgccatccatactcaattatcagaagatccatccagatccctgaagaagatcgctgt 1047
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Db    1098 GTTTACAGACAAGTTCATTCTATCATAAGACGTTCCTTGCCAGCAACACAAACTCAGTGT 1157

Qy    1048 tcccattccaagaaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgt 1107
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Db    1158 CATGTGGCAAACAAGACCTGTCCAAAAAATCATGTCTGGAATAATCAGATTTGCAGATGC 1217

Qy    1108 gttttgcaggaggaaaatccacttgctggaacagaagaccactctcatctccaggaacca 1167
           |    ||| | ||   |    |  ||          |   | ||| |       |||  |
Db    1218 TTAGCACAGCACGATTTTGGTTTCTCTTCTCACCTTGGAGATTCTGACACATCTGAAGGA 1277

Qy    1168 ---gctctctgtgggccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaaa 1224
              | | ||||||||  |||    | | || |||||    ||  | || |||||  |||
Db    1278 TTCCATATTTGTGGGCCCAACAAAGAGCTGGATGAAGAAACCTGTCAATGCGTCTGCAAA 1337
```

RESULT 15
T51371
ID T51371 standard; cDNA; 1674 BP.
AC T51371;
DT 23-APR-1997 (first entry)
DE Human vascular endothelial growth factor 2 cDNA.
KW Vascular endothelial growth factor 2; VEGF2; angiogenesis;
KW endothelialisation; coronary bypass surgery; vascular graft surgery;
KW agonist; antagonist; gene therapy; diagnosis; ds.
OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	cds	12. .1271
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FT	signal_peptide	12. .149
FT		/*tag= b
FT	mat_peptide	150. .1268
FT		/*tag= c
FT	primer_bind	complement (150. .166)
FT		/*tag= d
FT		/note= "5' primer binding site"
FT	primer_bind	1254. .1268
FT		/*tag= e
FT		/note= "3' primer binding site"
FT	primer_bind	1254. .1268
FT		/*tag= f
FT		/note= "3' primer binding site"

PN WO9639515-A1.
PD 12-DEC-1996.

PF 06-JUN-1996; U09001.
PR 06-JUN-1995; US-465968.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Cao L, Hu J, Rosen CA;
DR WPI; 97-043137/04.
DR P-PSDB; W11478.
PT DNA encoding human vascular endothelial growth factor 2 - used to
PT promote angiogenesis or endothelialisation in vascular graft surgery
PS Claim 1; Fig 1; 74pp; English.
CC A cDNA clone (T51371) codes for human vascular endothelial growth
CC factor 2 (VEGF2) (W11478), a protein structurally related to the
CC VEGF/PDGF family that is capable of inducing angiogenesis in vivo.
CC It was discovered in a cDNA library derived from early stage human
CC embryo week 9. VEGF2 polynucpeotides may also be obtd. from adult
CC heart or several breast cancer cell lines. VEGF2 nucleic acids
CC can be used in the prodn. of recombinant VEGF2, as probes to
CC detect mutations in the VEGF2, and in gene therapy to treat
CC patients in need of VEGF2. Antisense sequences can be used as
CC VEGF2 antagonists e.g. to inhibit growth of tumours.
SQ Sequence 1674 BP; 502 A; 384 C; 375 G; 413 T;

Query Match 6.4%; Score 129; DB 1; Length 1674;
Best Local Similarity 52.5%; Pred. No. 4.6e-28;
Matches 310; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

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Qy    642 ctcagcatcccatcggtccactaggtttgcggcaactttctatgacattgaaacactaaa 701
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Db    311 CTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAA 370

Qy    702 agttatagatgaagaatggcaaagaactcagtgcagccctagagaaacgtgcgtggaggt 761
          |  ||| ||| | || ||| ||  ||||| |||| ||  | ||   ||| | || ||
Db    371 AAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGT 430

Qy    762 ggccagtgagctggggaagagtaccaacacattcttcaagccccccttgtgtgaacgtgtt 821
          ||  |  ||| | ||       || ||||| ||||| || || || ||||||  ||| |
Db    431 GGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTA 490

Qy    822 ccgatgtggtggctgttgcaatgaagagagccttatctgtatgaacaccagcacctcgta 881
          | ||||||| || || ||||||   ||| | ||    || ||||||||||||||    ||
Db    491 CAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTA 550

Qy    882 catttccaaacagctctttgagatatcagtgcctttgacatcagtacctgaattagtgcc 941
          | |   |||   | | ||||| ||  |||||||| |  |   ||  ||  ||  |||  |
Db    551 CCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAAC 610

Qy    942 tgttaaagttgccaatcatacaggttgtaagtgcttgccaaca------gccccccgcca 995
            | |   |||||||||| ||    ||    ||| || | | |      |    | | ||
Db    611 AATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACA 670

Qy    996 tccatactcaattatcagaagatccatccagatccctgaagaagatcgctgttcccattc 1055
          |  || ||||| ||| | ||| | |      |   |  | |  |     |
Db    671 AGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAA 730

Qy   1056 caagaaactctgtcctattgacatgctatgggatagcaacaaatgtaaatgtgttttgca 1115
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Db    731 CAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGA 790

Qy   1116 ggaggaaaatccacttgctggaacagaagaccactctcatctccaggaaccagctctctg 1175
           ||    |         | |   | | |||  ||||          |  |   ||||
Db    791 AGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTG 850

Qy   1176 tgggccacacatgatgtttgacgaagatcgttgcgagtgtgtctgtaaaac 1226
          ||| ||| ||| |  | | || |||||    ||  |||||||||| | | |
Db    851 TGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAGC 901
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Search completed: May 16, 2000, 14:36:12
Job time: 9094 sec

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RX   MEDLINE; 99096474.
RA   LEI J., JIANG A., PEI D.;
RT   "Identification and characterization of a new splicing variant of
RT   vascular endothelial growth factor: VEGF183.";
RL   Biochim. Biophys. Acta, Gene Struct. Expr. 1443:400-406(1998).
RN   [2]
RP   SEQUENCE OF 114-209 FROM N.A.
RC   TISSUE=RETINA;
RA   JINGJING L., ROQUE R.S.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ010438; CAA09179.1; -.
DR   EMBL; AF062645; AAC16730.1; -.
DR   HSSP; P15692; 2VPF.
DR   PROSITE; PS00249; PDGF; 1.
KW   Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    209       VEGF183 PROTEIN.
SQ   SEQUENCE   209 AA;  24422 MW;  F2ABD204 CRC32;


  Query Match             10.2%;  Score 201;  DB 4;  Length 209;
  Best Local Similarity   25.6%;  Pred. No. 2.3e-11;
  Matches   57;  Conservative   25;  Mismatches   81;  Indels   60;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:| | |: |
Db      39 EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 97

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
             | |: |:  |       |     :  :    |  |:|                  |::
Db      98 EESNITMQIMRIK------PHQGQHIGEMSFLQHNKCECR-----------------PKK 134

Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||    ||         | : |          |       ::   |||
Db     135 DRARQEKK---------SVRGK----------GKGQKRKRKKSRPCGP------------ 164

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |        :| |: | |  || :   |  :    :  || |:
Db     164 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 205


RESULT  10
Q9XSF3
ID   Q9XSF3      PRELIMINARY;      PRT;   190 AA.
AC   Q9XSF3;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 164.
GN   VEGF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   JINGJING L., ROQUE R.S.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133248; AAD29682.1; -.
DR   PROSITE; PS00249; PDGF; 1.
SQ   SEQUENCE   190 AA;  22292 MW;  A0E1F28B CRC32;


  Query Match             10.1%;  Score 199;  DB 6;  Length 190;
  Best Local Similarity   24.2%;  Pred. No. 3.2e-11;
  Matches   54;  Conservative   25;  Mismatches   66;  Indels   78;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:| | |: |
Db      38 EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
             |: |:  |       |     :  :    |: |:|                  |::
Db      97 EEFNITMQIMRIK------PHQGQHIGEMSFLQHSKCECR-----------------PKK 133

Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||                          ::|||               |||
Db     134 DRA---------------------RQENP--------------CGP------------ 145

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |        :| |: | |  || :   |  :    :  || |:
Db     145 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT  11
O42572
ID   O42572      PRELIMINARY;      PRT;   194 AA.
AC   O42572;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 196.
GN   VEGF.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC   Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
OC   Xenopus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CLEAVER O., TONISSEN K.F., SAHA M.S., KRIEG P.A.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF008594; AAB63680.1; -.
DR   HSSP; P15692; 2VGH.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
SQ   SEQUENCE   194 AA;  22672 MW;  74B8253A CRC32;


  Query Match             10.1%;  Score 198.5;  DB 13;  Length 194;
  Best Local Similarity   21.4%;  Pred. No. 3.6e-11;
  Matches   57;  Conservative   34;  Mismatches   88;  Indels   87;  Gaps    9;

Qy      50 LEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRT 109
           |  || | |::          |     |      |: |        :: |||    ::|:
Db      12 LAVLLYIPHAQ----------LSGAAPMPG-EGDHKPTEV------VKFLKV----YERS 50

Qy     110 QCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEIS 169
           |  ||  |::  |         ||| || : || ||||:||| |: |    |: |: :|
Db      51 MCQVREILVDIFQEYPDEVEYIFKPSCVPLMRCAGCCNDESLECVPTECYNITMQIMKIK 110

Qy     170 VPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWD 229
             ::    :: :    |: |:| |          :: ::  :|: |
Db     111 PHISQ--HIMDMSFQQHSQCECRP----------KKEVKSKQENHC-------------- 145

Qy     230 SNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCS 289
                       |        ||                                :| |: |
Db     145 ----------EPCTEKSQRKHL--------------------------FVQDPQTCK 165

Qy     290 CFECKESLETCCQKHKLFHPDTCSCE 315
           |  || :   |  :    :  || ||
Db     166 C-SCKNTDSRCKTRQLELNERTCRCE 190


RESULT  12
Q94446
ID   Q94446      PRELIMINARY;      PRT;  1704 AA.
AC   Q94446;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   220 KDA SILK PROTEIN.
GN   SP220.
OS   Chironomus thummi thummi (Midge).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC   Chironomoidea; Chironomidae; Chironominae; Chironomus.
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RA   CASE S.T., COX C., BELL W.C., HOFFMAN R.T., MARTIN J., HAMILTON R.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U54641; AAA99804.1; -.
DR   HSSP; P04355; 4MT2.
DR   PRINTS; PR00876; MTNEMATODE.
SQ   SEQUENCE   1704 AA;  185745 MW;  0245A38E CRC32;


  Query Match             10.1%;  Score 198.5;  DB 5;  Length 1704;
  Best Local Similarity   21.7%;  Pred. No. 3.6e-10;
  Matches   73;  Conservative   42;  Mismatches   92;  Indels  129;  Gaps   17;

Qy     109 TQCSPRETCVEVASELGKSTNTFFKPPCVNVFR-----CGGCCNEESLICMNTSTSYISK 163
           | |  ::| :|   | |  |     :| |:: ||     ||  |:|:  |          |
Db    1079 TNCPAKQTFIESECECGCET----RPKCLDGFRFSNLECGCVCDEKK--CQ-------GK 1125

Qy     164 QLFEISVPLTSVP-----------ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPE 211
           |:|: :     |            :  ||  :    |||    | :        :|
Db    1126 QIFDKNTCKCKCPNEKPGDSCGKGKDFCPVDCS----CKCKSPKPANGCP----GVQEWN 1177

Qy     212 EDRC------SHSKKLCPIDMLWDSNKCKCVLQEENP-LAGTEDHSHLQEPALCGPHM-- 263
           ||:|      ||  |     |: |:|:|      |  : :: :|::     | | |
Db    1178 EDKCKCECPKDKSKTTCEGGQKWNDNQCQCGCPTPAPTCSASQKYSNVTCSCGCNPGMPA 1237

Qy     263 -------------------------------MFDEDRCECVCKTPCP----KDLIQHPK 286
                                         :::  ||| ||  ||     | : : .|
Db    1238 KGCPGNQVWCENSCQCVCPKNMEKPADNCGNKWWNDKACECECKPGCPEAGCKGVQKWNK 1297

Qy     287 N-CSCFECKESLET--CCQKHKLFHPDTCSCEDR-------CPFH-------------T 322
           | |:| ||     |   |   | ::||:|||: :       || :             |
Db    1298 NTCAC-ECPPGKATPASCGDKKSWNPDSCSCQCKSKMPGGGCPSNQQWNCETCKCECSGT 1356

Qy     323 RPCASGKT--------------------ACAKHCR 337
           : | :|::                     ||| |:
Db    1357 QTCPAGQSWDSQTCQCSCPATGKCTGAQFWCAKQCK 1392


RESULT  13
Q9XSF4
ID   Q9XSF4       PRELIMINARY;      PRT;   208 AA.
AC   Q9XSF4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 182.
GN   VEGF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   JINGJING L., ROQUE R.S.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133249; AAD29683.1; -.
DR   PROSITE; PS00249; PDGF; 1.
SQ   SEQUENCE   208 AA;  24400 MW;  A8266335 CRC32;


  Query Match             10.0%;  Score 196;  DB 6;  Length 208;
  Best Local Similarity   25.1%;  Pred. No. 6.7e-11;
  Matches   56;  Conservative   26;  Mismatches   81;  Indels   60;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |           ||| || : ||||||:| | |: |
Db      38 EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
           |: |:  |       |    :  :    |: |:|                      |::
Db      97 EEFNITMQIMRIK------PHQGQHIGEMSFLQHSKCECR----------------PKK 133


Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||    ||          | : |           |       ::   |||
Db     134 DRARQEKK---------SVRGK----------GKGQKRKRKKSRPCGP---------- 163

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |         :| |: | |  || :   |  :    :  || |:
Db     163 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 204


RESULT  14
O75875
ID   O75875       PRELIMINARY;      PRT;   191 AA.
AC   O75875;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST;
RX   MEDLINE; 98119755.
RA   CLAFFEY K.P., SHIH S.-C., MULLEN A., DZIENNIS S., CUSICK J.L.,
RA   ABRAMS K.R., LEE S.W., DETMAR M.;
RT   "Identification of a human VPF/VEGF 3' untranslated region mediating
RT   hypoxia-induced mRNA stability.";
RL   Mol. Biol. Cell 9:469-481(1998).
DR   EMBL; AF022375; AAC63143.1; -.
DR   HSSP; P15692; 1VPP.
DR   PFAM; PF00341; PDGF; 1.
SQ   SEQUENCE   191 AA;  22320 MW;  3D6B10B2 CRC32;


  Query Match             9.9%;  Score 195;  DB 4;  Length 191;
  Best Local Similarity   24.2%;  Pred. No. 7.6e-11;
  Matches   54;  Conservative   24;  Mismatches   67;  Indels   78;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |           ||| || : ||||| |:| | |: |
Db      39 EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCSNDEGLECVPT 97

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
           | |: |:  |       |    :  :    |  |:|                      |::
Db      98 EESNITMQIMRIK------PHQGQHIGEMSFLQHNKCECR----------------PKK 134

Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||                    ::|||                 |||
Db     135 DRA---------------------RQENP--------------CGP---------- 146

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |         :| |: | |  || :   |  :    :  || |:
Db     146 CSERRKHLFVQDPQTCKC-SCKNTHSRCKARQLELNERTCRCD 187


RESULT  15
Q9XSF5
ID   Q9XSF5       PRELIMINARY;      PRT;   214 AA.
AC   Q9XSF5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 188.
GN   VEGF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   JINGJING L., ROQUE R.S.;
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RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133250; AAD29684.1; -.
DR   PROSITE; PS00249; PDGF; 1.
SQ   SEQUENCE   214 AA;  25151 MW;  84CD48B8 CRC32;


  Query Match             9.7%;  Score 191;  DB 6;  Length 214;
  Best Local Similarity   25.1%;  Pred. No. 2e-10;
  Matches   56;  Conservative   27;  Mismatches   86;  Indels   54;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:| | |: |
Db      38 EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
               |: |:  |       |     :  :    |: |:|                 |::
Db      97 EEFNITMQIMRIK------PHQGQHIGEMSFLQHSKCECR----------------PKK 133

Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||    ||         | : |   |:       :   :      |||
Db     134 DRARQEKK---------SVRGKGKGQKRK----RKKSRYKSWSVPCGP------------ 169

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |        :| |: | |  || :   |  :    :  || |:
Db     169 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 210


Search completed: May 16, 2000, 16:41:32
Job time: 6556 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 16, 2000, 12:32:20 ; Search time 32.09 Seconds
(without alignments)
261.293 Million cell updates/sec

Title: US-09-214-982-1
Perfect score: 1963
Sequence: 1 MYREWVVVNVFMMLYVQLVQ.....HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1963	100.0	354	1	W44293	Human vascular end
2	1963	100.0	354	1	W53241	Homo sapiens vascu
3	1963	100.0	354	1	W49036	Human zvegf2 growt
4	1917	97.7	620	1	W14994	Human c-Fos induce
5	1804	91.9	325	1	W53240	Homo sapiens vascu
6	1675	85.3	358	1	W44295	Mouse vascular end
7	1675	85.3	358	1	W53242	Mus musculus vascu
8	1671	85.1	358	1	W14992	Murine c-Fos induc
9	1522	77.5	321	1	W53243	Mus musculus vascu
10	1517.5	77.3	326	1	W44296	Rat vascular endot
11	706.5	36.0	419	1	W11478	Human vascular end
12	704.5	35.9	399	1	W86237	Human VEGF-C full
13	704.5	35.9	419	1	W00932	Human Flt4 recepto
14	704.5	35.9	419	1	W17837	Human foetal liver
15	704.5	35.9	419	1	W75740	Human vascular end
16	704.5	35.9	419	1	W86203	Human vascular end
17	696	35.5	415	1	W00933	Mouse Flt4 recepto
18	696	35.5	415	1	W75742	Mouse vascular end
19	695.5	35.4	419	1	W13833	Human vascular end
20	693.5	35.3	419	1	W75751	Vascular endotheli
21	677	34.5	418	1	W00934	Quail Flt4 recepto
22	677	34.5	418	1	W75743	Quail vascular end
23	659.5	33.6	350	1	R82686	Vascular endotheli
24	615.5	31.4	307	1	W86222	Human VEGF-C trunc
25	604.5	30.8	302	1	W86223	Human VEGF-C trunc
26	593.5	30.2	297	1	W86224	Human VEGF-C trunc
27	570.5	29.1	292	1	W86225	Human VEGF-C trunc
28	212.5	10.8	588	1	W00592	SAP-AlaMet-VEGF165
29	210	10.7	598	1	R94074	SAP(Gly4Ser)VEGF16
30	207	10.5	594	1	W00591	SAP-AlaMet-VEGF165
31	207	10.5	595	1	W00595	SAP-GlySer-VEGF165
32	205.5	10.5	192	1	R94040	VEGF165 Cys+2. Vas
33	205	10.4	165	1	W31086	Vascular endotheli
34	204.5	10.4	600	1	W00593	SAP-AlaMet-VEGF165
35	204.5	10.4	612	1	W00596	SAP(Gly4Ser)2VEGF1
36	204	10.4	165	1	R38921	Human VEGF-165. Is
37	204	10.4	191	1	R08002	Human vascular end
38	204	10.4	191	1	R91076	Human vascular end
39	204	10.4	191	1	R94002	VEGF165. Vascular
40	204	10.4	191	1	W00724	Vascular endotheli
41	204	10.4	191	1	W38242	Vascular endotheli
42	204	10.4	191	1	W69331	Human VEGF protein
43	204	10.4	191	1	Y07725	Human VEGF protein
44	204	10.4	192	1	R94039	VEGF165 Cys+4. Vas
45	204	10.4	421	1	W00584	SAP-AlaMet-VEGF165

ALIGNMENTS

RESULT 1
W44293
ID W44293 standard; Protein; 354 AA.
AC W44293;
DT 22-JUN-1998 (first entry)
DE Human vascular endothelial growth factor D.
KW Human; vascular endothelial growth factor D; VEGF-D; gene therapy;
KW inflammation; oedema.
OS Homo sapiens.
PN WO9802543-A1.
PD 22-JAN-1998.
PF 15-JUL-1997; J02456.
PR 15-JUL-1996; JP-185216.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PI Hirata Y, Nezu J;
DR WPI; 98-110591/10.
DR N-PSDB; V15156.
PT VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT treating oedema
PS Claim 1; Page 18-20; 52pp; Japanese.
CC The present sequence represents human vascular endothelial growth factor
CC D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC the protein, may be useful in, e.g. gene therapy and in treatment of
CC inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
CC DNA sequences may be used for screening for the compounds which bind to
CC the VEGF-D protein.
SQ Sequence 354 AA;

Query Match 100.0%; Score 1963; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60

Qy      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120

Qy     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180

Qy     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240

Qy     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300

Qy     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
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RESULT   2
W53241
ID   W53241 standard; Protein; 354 AA.
AC   W53241;
DT   03-AUG-1998  (first entry)
DE   Homo sapiens vascular endothelial growth factor D (VEGF-D).
KW   vascular endothelial growth factor; VEGF-D; angiogenesis;
KW   modification; acceleration; wound healing; tissue; organ;
KW   transplants; collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW   detection; diagnosis; congestive heart failure.
OS   Homo sapiens.
PN   WO9807832-A1.
PD   26-FEB-1998.
PF   21-AUG-1997; U14696.
PR   01-JUL-1997; US-051426.
PR   23-AUG-1996; AU-001825.
PR   23-AUG-1996; US-023751.
PR   11-NOV-1996; AU-003554.
PR   14-NOV-1996; US-031097.
PR   05-FEB-1997; AU-004954.
PR   10-FEB-1997; US-038814.
PR   19-JUN-1997; AU-007435.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR   WPI; 98-179057/16.
DR   N-PSDB; V20807.
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung,
PT   heart or intestinal disorders
PS   Claim 16; Pages 60-61; 101pp; English.
CC   The sequence is that of human lung vascular endothelial growth factor
CC   D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis
CC   in wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis,
CC   such as coronary artery disease, and inhibition of angiogenesis in
CC   the treatment of cancer or of diabetic retinopathy.  It can also be
CC   used in the treatment of lung disorders to improve blood circulation
CC   in the lung and/or gaseous exchange between the lungs and the blood
CC   stream or to improve blood circulation to the heart and O2 gas
CC   permeability in cases of cardiac insufficiency, to improve blood
CC   flow and gaseous exchange in chronic obstructive airway disease,
CC   or to treat malabsorptive syndromes in the intestinal tract.
CC   Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC   as an indicator of future metastatic risk. Antagonists can be used
CC   for treating e.g. conditions such as congestive heart failure,
CC   involving accumulations of fluid in the lung resulting from
CC   increases in vascular permeability.  The products can also be used
CC   for detection and diagnosis.
SQ   Sequence   354 AA;


  Query Match           100.0%;  Score 1963;  DB 1;  Length 354;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-150;
  Matches  354;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60

Qy      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120

Qy     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180

Qy     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240

Qy     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300

Qy     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354


RESULT   3
W49036
ID   W49036 standard; Protein; 354 AA.
AC   W49036;
DT   26-OCT-1998  (first entry)
DE   Human zvegf2 growth factor.
KW   Human zvegf2 growth factor; mitogen; fibroblast; smooth muscle cell;
KW   venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect;
KW   angiogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis;
KW   scleroderma.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /note= "Signal peptide"
FT   Peptide         24. .108
FT                   /note= "Pro-region"
FT   Binding_site    109. .197
FT                   /note= "Receptor binding domain"
FT   Region          206. .256
FT                   /note= "Cysteine-rich domain"
FT   Region          257. .274
FT                   /note= "Balbiani ring motif"
FT   Region          275. .294
FT                   /note= "Balbiani ring motif"
FT   Region          295. .354
FT                   /note= "Cysteine-rich domain""
PN   WO9824811-A2.
PD   11-JUN-1998.
PF   20-NOV-1997; U20888.
PR   18-SEP-1997; US-933455.
PR   06-DEC-1996; US-759657.
PA   (ZYMO ) ZYMOGENETICS INC.
PI   Conklin DC, Gilbert T, Hart CE, Nygaard S, Sheppard PO;
DR   WPI; 98-333256/29.
DR   N-PSDB; V32823.
PT   New isolated vascular endothelial growth factor - used to develop
PT   products for treating e.g. wounds, burns, myocardial infarction,
PT   tumours, psoriasis, arthritis, restenosis or organ transplants
PS   Claim 1; Pages 53-54; 77pp; English.
CC   The present sequence represents a human zvegf2 growth factor encoded
CC   by the zvegf2 cDNA which was isolated from a human heart cDNA library.
CC   zvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or
CC   smooth muscle cells.  zvegf2 is claimed to be useful for stimulating the
CC   revascularisation of tissue or the re-endothelialisation of vascular
CC   tissue.  zvefg2 is particularly claimed to be useful for the treatment
CC   of full-thickness skin wounds, including venous stasis ulcers and
CC   diabetic ulcers.  The zvegf2 protein is also claimed to be useful as an
CC   additive in tissue adhesives for promoting revascularisation of the
CC   healing tissue.  Antagonists against zvegf2 can be used to block its
CC   mitogenic, chemotactic and angiogenic effects.  The antagonists may
CC   therefore be useful for reducing growth of solid tumours by inhibiting
CC   neovascularisation of the developing tumour or by directly blocking
CC   tumour cell growth, in the treatment of diabetic retinopathy, psoriasis,
CC   arthritis, and scleroderma.
SQ   Sequence   354 AA;


  Query Match           100.0%;  Score 1963;  DB 1;  Length 354;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-150;
  Matches  354;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60

Qy      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120

Qy     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180

Qy     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240

Qy     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300

Qy     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354


RESULT   4
W14994
ID   W14994 standard; Protein; 620 AA.
AC   W14994;
DT   05-JUL-1997  (first entry)
DE   Human c-Fos induced growth factor (clone HF175 ORF2 product).
KW   c-Fos induced frowth factor; FIGF; Fos regulated gene;
KW   proto-oncogene; lung disorder; cancer; tumour; therapy;
KW   antibody; transgenic animal.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   misc_difference 16
FT                   /note= "residue 16 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 26
FT                   /note= "residue 26 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 29
FT                   /note= "residue 29 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 47
FT                   /note= "residue 47 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 71
FT                   /note= "residue 71 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 72
FT                   /note= "residue 72 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 76
FT                   /note= "residue translated from ORF2 of HF175
FT                   is Ile"
FT   misc_difference 136
FT                   /note= "residue translated from ORF2 of HF175
FT                   is Ile"
FT   misc_difference 220
FT                   /note= "residue translated from ORF2 of HF175
FT                   is Phe"
FT   misc_difference 341
FT                   /note= "residue translated from ORF2 of HF175
FT                   is His"
FT   misc_difference 344
FT                   /note= "residue translated from ORF2 of HF175
FT                   is Phe"
FT   misc_difference 377
FT                   /note= "residue translated from ORF2 of HF175
FT                   is Leu"
FT   misc_difference 435
FT                   /note= "residue 435 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 486
FT                   /note= "residue 486 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 497
FT                   /note= "residue 497 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 518
FT                   /note= "residue 518 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 541
FT                   /note= "residue 541 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 553
FT                   /note= "residue 553 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 557
FT                   /note= "residue 557 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 562
FT                   /note= "residue 562 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 579
FT                   /note= "residue 579 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 592
FT                   /note= "residue 592 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 593
FT                   /note= "residue 593 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 597
FT                   /note= "residue 597 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 605
FT                   /note= "residue 605 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
FT   misc_difference 608
FT                   /note= "residue 608 corresponds to an in-frame
FT                   stop codon in reading frame 2 of HF175"
PN   WO9712972-A2.
PD   10-APR-1997.
PF   30-SEP-1996; IB1113.
PR   29-SEP-1995; GB-019928.
PR   13-JUN-1996; GB-012368.
PA   (UYSI-) UNIV SIENA.
PI   Oliviero S;
DR   WPI; 97-226216/20.
DR   N-PSDB; T62961.
PT   Nucleotide molecule encoding c-Fos induced growth factor protein -
PT   useful in therapy, in manufacture of compositions for treatment of
PT   developmental disorders and in generation of transgenic animal
PS   Claim 3; Fig 2; 64pp; English.
CC   3 Polypeptide sequences (W14993-95) are the respective translated
CC   sequences of reading frames 1, 2 and 3 of clone HF175 (T62961), the
CC   human homologue of murine clone F0401 (T62960), which codes for a
CC   novel c-Fos induced growth factor (FIGF) (see also W14992).
CC   Examination of the 3 polypeptides indicates that reading frame 2
CC   has the longest region free of nonsense codons.  FIGF is a c-fos-
CC   dependent autocrine growth factor able to induce cell division
CC   entry and, when over-expressed, a transformed phenotype in
CC   fibroblasts.  It could be implicated in tumours and development.
CC   Recombinant FIGF can be produced in transformed host (e.g. CHO)
CC   cells.  It can be used to identify its receptors and in an assay
CC   for the identification of agonists and antagonists.  Antibodies
CC   raised against FIGF can be used to block the function of the
CC   protein and thereby inhibit or suppress tumour growth.  Transgenic
CC   animals expressing FIGF can be generated for use e.g. as models for
CC   research.
SQ   Sequence   620 AA;
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  Query Match             97.7%;  Score 1917;  DB 1;  Length 620;
  Best Local Similarity   98.0%;  Pred. No. 1.6e-146;
  Matches  347;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      81 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRTTHSE 140

Qy      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 200

Qy     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180
           |||||||||||||||||| |||||||||| :|||||||||||||||||||||||||||||
Db     201 ASELGKSTNTFFKPPCVNVERCGGCCNEESFMCMNTSTSYISKQLFEISVPLTSVPELVP 260

Qy     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 320

Qy     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300
           |||||||||||||||||| || |||||||||||||||||||||||||||||| |||
Db     321 NPLAGTEDHSHLQEPALCGPDMMEDEDRCECVCKTPCPKDLIQHPKNCSCFECKESEETC 380

Qy     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     381 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 434


RESULT   5
W53240
ID   W53240 standard; Protein; 325 AA.
AC   W53240;
DT   03-AUG-1998  (first entry)
DE   Homo sapiens vascular endothelial growth factor D (VEGF-D).
KW   vascular endothelial growth factor; VEGF-D; angiogenesis;
KW   modification; acceleration; wound healing; tissue; organ;
KW   transplants; collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW   detection; diagnosis; congestive heart failure.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Region          126. .128
FT                   /note= "potential N-linked glycosylation site"
FT   Region          156. .158
FT                   /note= "potential N-linked glycosylation site"
FT   Region          258. .260
FT                   /note= "potential N-linked glycosylation site"
PN   WO9807832-A1.
PD   26-FEB-1998.
PF   21-AUG-1997; U14696.
PR   01-JUL-1997; US-051426.
PR   23-AUG-1996; AU-001825.
PR   23-AUG-1996; US-023751.
PR   11-NOV-1996; AU-003554.
PR   14-NOV-1996; US-031097.
PR   05-FEB-1997; AU-004954.
PR   10-FEB-1997; US-038814.
PR   19-JUN-1997; AU-007435.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR   WPI; 98-179057/16.
DR   N-PSDB; V20806.
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung,
PT   heart or intestinal disorders
PS   Claim 16; Pages 57-58; 101pp; English.
CC   The sequence is that of human breast vascular endothelial growth factor
CC   D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis
CC   in wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis,
CC   such as coronary artery disease, and inhibition of angiogenesis in
CC   the treatment of cancer or of diabetic retinopathy.  It can also be
CC   used in the treatment of lung disorders to improve blood circulation
CC   in the lung and/or gaseous exchange between the lungs and the blood
CC   stream or to improve blood circulation to the heart and O2 gas
CC   permeability in cases of cardiac insufficiency, to improve blood
CC   flow and gaseous exchange in chronic obstructive airway disease,
CC   or to treat malabsorptive syndromes in the intestinal tract.
CC   Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC   as an indicator of future metastatic risk. Antagonists can be used
CC   for treating e.g. conditions such as congestive heart failure,
CC   involving accumulations of fluid in the lung resulting from
CC   increases in vascular permeability.  The products can also be used
CC   for detection and diagnosis.
SQ   Sequence   325 AA;


  Query Match             91.9%;  Score 1804;  DB 1;  Length 325;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-138;
  Matches  324;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      31 RSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFA 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 RSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFA 61

Qy      91 ATFYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEES 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 ATFYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEES 121

Qy     151 LICMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIP 210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 LICMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIP 181

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCE 270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 EEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCE 241

Qy     271 CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKT 330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKT 301

Qy     331 ACAKHCRFPKEKRAAQGPHSRKNP 354
           ||||||||||||||||||||||||
Db     302 ACAKHCRFPKEKRAAQGPHSRKNP 325


RESULT   6
W44295
ID   W44295 standard; Protein; 358 AA.
AC   W44295;
DT   22-JUN-1998  (first entry)
DE   Mouse vascular endothelial growth factor D.
KW   Mouse; vascular endothelial growth factor D; VEGF-D; gene therapy;
KW   inflammation; oedema.
OS   Mus sp.
PN   WO9802543-A1.
PD   22-JAN-1998.
PF   15-JUL-1997; J02456.
PR   15-JUL-1996; JP-185216.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PI   Hirata Y, Nezu J;
DR   WPI; 98-110591/10.
DR   N-PSDB; V15177.
PT   VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT   treating oedema
PS   Example 7; Page 32-35; 52pp; Japanese.
CC   The present sequence represents mouse vascular endothelial growth factor
CC   D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC   the protein, may be useful in, e.g. gene therapy and in treatment of
CC   inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
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CC   DNA sequences may be used for screening for the compounds which bind to
CC   the VEGF-D protein.
SQ   Sequence   358 AA;


  Query Match             85.3%;  Score 1675;  DB 1;  Length 358;
  Best Local Similarity   83.8%;  Pred. No. 2.4e-127;
  Matches  301;  Conservative   20;  Mismatches   32;  Indels    6;  Gaps    2;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
           || || : |: || :| ||||  :|||||     |||:| ||||||||||||||||||:
Db       1 MYGEWGMGNILMMFHVYLVQGFRSEHGPVKDFSFERSSRSMLERSEQQIRAASSLEELLQ 60

Qy      56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           | ||||||||||||:|||  ||||||||||||||||||| ||||||||||||||||||||
Db      61 IAHSEDWKLWRCRLKLKSLASMDSRSASHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE 120

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
           |||||||||||:|||||||||||||||||||| ::|||||||||||||||||||||||||
Db     121 TCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEEGVMCMNTSTSYISKQLFEISVPLTSV 180

Qy     176 PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC 235
           |||||||:|||||||||| |||||||||||| |||||||||||||: ||||
Db     181 PELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC 240

Qy     236 VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKE 295
           |||:| || ||||||:|||| |||||| |||||||||| ||| ||||||:||||||||
Db     241 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKAPCPGDLIQHPENCSCFECKE 300

Qy     296 SLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           |||:|||||:|||||||||||||||| ||| | || || ||||| | ||| :|::||
Db     301 SLESCCQKHKIFHPDTCSCEDRCPFHTRTCASRKPACGKHWRFPKETR-AQGLYSQENP 358


RESULT   7
W53242
ID   W53242 standard; Protein; 358 AA.
AC   W53242;
DT   03-AUG-1998  (first entry)
DE   Mus musculus vascular endothelial growth factor D1 (VEGF-D1).
KW   vascular endothelial growth factor; VEGF-D; angiogenesis;
KW   modification; acceleration; wound healing; tissue; organ;
KW   transplants; collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW   detection; diagnosis; congestive heart failure.
OS   Mus musculus.
PN   WO9807832-A1.
PD   26-FEB-1998.
PF   21-AUG-1997; U14696.
PR   01-JUL-1997; US-051426.
PR   23-AUG-1996; AU-001825.
PR   23-AUG-1996; US-023751.
PR   11-NOV-1996; AU-003554.
PR   14-NOV-1996; US-031097.
PR   05-FEB-1997; AU-004954.
PR   10-FEB-1997; US-038814.
PR   19-JUN-1997; AU-007435.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR   WPI; 98-179057/16.
DR   N-PSDB; V20808.
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung,
PT   heart or intestinal disorders
PS   Claim 16; Pages 63-64; 101pp; English.
CC   The sequence is that of mouse lung vascular endothelial growth factor
CC   D1 (VEGF-D1). VEGF-D1 can be used for e.g. acceleration of angiogenesis
CC   in wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis,
CC   such as coronary artery disease, and inhibition of angiogenesis in
CC   the treatment of cancer or of diabetic retinopathy.  It can also be
CC   used in the treatment of lung disorders to improve blood circulation
CC   in the lung and/or gaseous exchange between the lungs and the blood
CC   stream or to improve blood circulation to the heart and O2 gas
CC   permeability in cases of cardiac insufficiency, to improve blood
CC   flow and gaseous exchange in chronic obstructive airway disease,
CC   or to treat malabsorptive syndromes in the intestinal tract.
CC   Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC   as an indicator of future metastatic risk. Antagonists can be used
CC   for treating e.g. conditions such as congestive heart failure,
CC   involving accumulations of fluid in the lung resulting from
CC   increases in vascular permeability.  The products can also be used
CC   for detection and diagnosis.
SQ   Sequence   358 AA;


  Query Match             85.3%;  Score 1675;  DB 1;  Length 358;
  Best Local Similarity   83.8%;  Pred. No. 2.4e-127;
  Matches  301;  Conservative   20;  Mismatches   32;  Indels    6;  Gaps    2;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
           || || : |: || :| ||||  :|||||     |||:| ||||||||||||||||||:
Db       1 MYGEWGMGNILMMFHVYLVQGFRSEHGPVKDFSFERSSRSMLERSEQQIRAASSLEELLQ 60

Qy      56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           | ||||||||||||:|||  ||||||||||||||||||| ||||||||||||||||||||
Db      61 IAHSEDWKLWRCRLKLKSLASMDSRSASHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE 120

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
           |||||||||||:|||||||||||||||||||| ::|||||||||||||||||||||||||
Db     121 TCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEEGVMCMNTSTSYISKQLFEISVPLTSV 180

Qy     176 PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC 235
           |||||||:|||||||||| |||||||||||| |||||||||||||: ||||
Db     181 PELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC 240

Qy     236 VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKE 295
           |||:| || ||||||:|||| |||||| |||||||||| ||| ||||||:||||||||
Db     241 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKAPCPGDLIQHPENCSCFECKE 300

Qy     296 SLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           |||:|||||:|||||||||||||||| ||| | || || ||||| | ||| :|::||
Db     301 SLESCCQKHKIFHPDTCSCEDRCPFHTRTCASRKPACGKHWRFPKETR-AQGLYSQENP 358


RESULT   8
W14992
ID   W14992 standard; Protein; 358 AA.
AC   W14992;
DT   05-JUL-1997  (first entry)
DE   Murine c-Fos induced growth factor.
KW   c-Fos induced frowth factor; FIGF; Fos regulated gene;
KW   proto-oncogene; lung disorder; cancer; tumour; therapy;
KW   antibody; transgenic animal.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   region          112. .164
FT                   /note= "VEGF homology region"
PN   WO9712972-A2.
PD   10-APR-1997.
PF   30-SEP-1996; IB1113.
PR   29-SEP-1995; GB-019928.
PR   13-JUN-1996; GB-012368.
PA   (UYSI-) UNIV SIENA.
PI   Oliviero S;
DR   WPI; 97-226216/20.
DR   N-PSDB; T62960.
PT   Nucleotide molecule encoding c-Fos induced growth factor protein -
PT   useful in therapy, in manufacture of compositions for treatment of
PT   developmental disorders and in generation of transgenic animal
PS   Claim 3; Fig 1; 64pp; English.
CC   Novel murine c-Fos induced growth factor (FIGF) (W14992) shows
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CC   homology to the growth factor VEGF.  It is encoded by the F0401
CC   gene (T62960) obtd. from mouse fibroblast cells.  FIGF is a c-fos-
CC   dependent autocrine growth factor able to induce cell division
CC   entry and, when over-expressed, a transformed phenotype in
CC   fibroblasts.  It could be implicated in tumours and development.
CC   Recombinant FIGF can be produced in transformed host (e.g. CHO)
CC   cells.  It can be used to identify its receptors and in an assay
CC   for the identification of agonists and antagonists.  Antibodies
CC   raised against FIGF can be used to block the function of the
CC   protein and thereby inhibit or suppress tumour growth.  Transgenic
CC   animals expressing FIGF can be generated for use e.g. as models for
CC   research.
SQ   Sequence   358 AA;


  Query Match             85.1%;  Score 1671;  DB 1;  Length 358;
  Best Local Similarity   83.6%;  Pred. No. 5.1e-127;
  Matches  300;  Conservative   21;  Mismatches   32;  Indels    6;  Gaps    2;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
           || || : |: || :| ||||  :||||||     |||:| ||||||||||||||||||:
Db       1 MYGEWGMGNILMMFHVYLVQGFRSEHGPVKDFSFERSSRSMLERSEQQIRAASSLEELLQ 60

Qy      56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           | ||||||||||||:|||  ||:||||||||||||||| ||||||||||||||||||||
Db      61 IAHSEDWKLWRCRLKLKSLASMESRSASHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE 120

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
           ||||||||||:|||||||||||||||||| ::|||||||||||||||||||||||||||||
Db     121 TCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEEGVMCMNTSTSYISKQLFEISVPLTSV 180

Qy     176 PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC 235
           |||||||:|||||||||||| |||||||||||| |||| | ||||||||||||: ||||
Db     181 PELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC 240

Qy     236 VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKE 295
           |||:| || |||||||:|||| |||||| |||||||||| ||| ||||||:|||||||||
Db     241 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKAPCPGDLIQHPENCSCFECKE 300

Qy     296 SLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           |||:||||||:|||||||||||||||| ||| | || || ||||| | ||| :|::||
Db     301 SLESCCQKHKIFHPDTCSCEDRCPFHTRTCASRKPACGKHWRFPKETR-AQGLYSQENP 358


RESULT   9
W53243
ID   W53243 standard; Protein; 321 AA.
AC   W53243;
DT   03-AUG-1998  (first entry)
DE   Mus musculus vascular endothelial growth factor D2 (VEGF-D2).
KW   vascular endothelial growth factor; VEGF-D; angiogenesis;
KW   modification; acceleration; wound healing; tissue; organ;
KW   transplants; collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk;
KW   detection; diagnosis; congestive heart failure.
OS   Mus musculus.
PN   WO9807832-A1.
PD   26-FEB-1998.
PF   21-AUG-1997; U14696.
PR   01-JUL-1997; US-051426.
PR   23-AUG-1996; AU-001825.
PR   23-AUG-1996; US-023751.
PR   11-NOV-1996; AU-003554.
PR   14-NOV-1996; US-031097.
PR   05-FEB-1997; AU-004954.
PR   10-FEB-1997; US-038814.
PR   19-JUN-1997; AU-007435.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA,  (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Achen MG, Alitalo K, Stacker SA, Wilks AF;
DR   WPI; 98-179057/16.
DR   N-PSDB; V20809.
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung,
PT   heart or intestinal disorders
PS   Claim 16; Pages 64-65; 101pp; English.
CC   The sequence is that of mouse lung vascular endothelial growth factor
CC   D2 (VEGF-D2). VEGF-D2 can be used for e.g. acceleration of angiogenesis
CC   in wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis,
CC   such as coronary artery disease, and inhibition of angiogenesis in
CC   the treatment of cancer or of diabetic retinopathy.  It can also be
CC   used in the treatment of lung disorders to improve blood circulation
CC   in the lung and/or gaseous exchange between the lungs and the blood
CC   stream or to improve blood circulation to the heart and O2 gas
CC   permeability in cases of cardiac insufficiency, to improve blood
CC   flow and gaseous exchange in chronic obstructive airway disease,
CC   or to treat malabsorptive syndromes in the intestinal tract.
CC   Quantitation of VEGF-D in cancer biopsy specimens may be useful
CC   as an indicator of future metastatic risk. Antagonists can be used
CC   for treating e.g. conditions such as congestive heart failure,
CC   involving accumulations of fluid in the lung resulting from
CC   increases in vascular permeability.  The products can also be used
CC   for detection and diagnosis.
SQ   Sequence   321 AA;


  Query Match             77.5%;  Score 1522;  DB 1;  Length 321;
  Best Local Similarity   86.5%;  Pred. No. 4.3e-115;
  Matches  270;  Conservative   17;  Mismatches   25;  Indels    0;  Gaps    0;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
           || || : |: || :| ||||  :|||||||||:| ||||||||||||||||||:| |||
Db       1 MYGEWGMGNILMMFHVYLVQGFRSEHGPVKRSSRSMLERSEQQIRAASSLEELLQIAHSE 60

Qy      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120
           ||||||||||:|||  |||||||||||||||||||| ||||||||||||||||||||||||
Db      61 DWKLWRCRLKLKSLASMDSRSASHRSTRFAATFYDTETLKVIDEEWQRTQCSPRETCVEV 120

Qy     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180
           |||||||:|||||||||||||||||||| ::|||||||||||||||||||||||||||||||
Db     121 ASELGKTTNTFFKPPCVNVFRCGGCCNEEGVMCMNTSTSYISKQLFEISVPLTSVPELVP 180

Qy     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240
           ||:|||||||||| |||||||||||| |||| | ||||||||||||: |||||||:|
Db     181 VKIANHTGCKCLPTGPRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKCVLQDE 240

Qy     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300
           || ||||||:|||| |||||| |||||||||| ||| ||||||:||||||||||||:|
Db     241 TPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKAPCPGDLIQHPENCSCFECKESLESC 300

Qy     301 CQKHKLFHPDTC 312
           |||||:||||||
Db     301 CQKHKIFHPDTC 312


RESULT  10
W44296
ID   W44296 standard; Protein; 326 AA.
AC   W44296;
DT   22-JUN-1998  (first entry)
DE   Rat vascular endothelial growth factor D.
KW   Rate; vascular endothelial growth factor D; VEGF-D; gene therapy;
KW   inflammation; oedema.
OS   Rattus sp.
PN   WO9802543-A1.
PD   22-JAN-1998.
PF   15-JUL-1997; J02456.
PR   15-JUL-1996; JP-185216.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PI   Hirata Y, Nezu J;
DR   WPI; 98-110591/10.
DR   N-PSDB; V15178.
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PT   VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT   treating oedema
PS   Example 8; Page 35-38; 52pp; Japanese.
CC   The present sequence represents rat vascular endothelial growth factor D
CC   (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC   the protein, may be useful in, e.g. gene therapy and in treatment of
CC   inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
CC   DNA sequences may be used for screening for the compounds which bind to
CC   the VEGF-D protein.
SQ   Sequence   326 AA;


  Query Match             77.3%;  Score 1517.5;  DB 1;  Length 326;
  Best Local Similarity   85.2%;  Pred. No. 1e-114;
  Matches  270;  Conservative   20;  Mismatches   22;  Indels    5;  Gaps    1;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
           || ||  ||: || || |||| | ||  ||      |||:| ||||||||||||:|||||:
Db       1 MYGEWAAVNILMMSYVYLVQGFSIEHRAVKDVSLERSSRSVLERSEQQIRAASTLEELLQ 60

Qy      56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           : |||||||||||:|||  ::|||| |||||||||||| ||||||||||||||||||||
Db      61 VAHSEDWKLWRCRLKLKSLANVDSRSTSHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE 120

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
           ||||||||||:|||||||||||||||||||||::|||||||||||||||||||||||||||
Db     121 TCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEESVMCMNTSTSYISKQLFEISVPLTSV 180

Qy     176 PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC 235
           |||||||:|||||||||| ||||||||||||||||:| |||||||:|||||: ||||
Db     181 PELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQIPEEDQCPHSKKLCPVDMLWDNTKCKC 240

Qy     236 VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKE 295
           |||:|||| |||||||:|||||||||||||||||||||| ||| ||||||:|||||||||
Db     241 VLQDENPLPGTEDHSYLQEPALCGPHMMFDEDRCECVCKAPCPGDLIQHPENCSCFECKE 300

Qy     296 SLETCCQKHKLFHPDTC 312
           |||:|||||||:||||||
Db     301 SLESCCQKHKMFHPDTC 317


RESULT  11
W11478
ID   W11478 standard; Protein; 419 AA.
AC   W11478;
DT   23-APR-1997  (first entry)
DE   Human vascular endothelial growth factor 2.
KW   Vascular endothelial growth factor 2; VEGF2; angiogenesis;
KW   endothelialisation; coronary bypass surgery; vascular graft surgery;
KW   agonist; antagonist; therapy; diagnosis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1. .46
FT                   /label= Sig_peptide
FT   protein         47. .419
FT                   /label= Mat_protein
FT                   /note= "the mature protein is separately claimed
FT                   (Claim 5)"
PN   WO9639515-A1.
PD   12-DEC-1996.
PF   06-JUN-1996; U09001.
PR   06-JUN-1995; US-465968.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Cao L,  Hu J,  Rosen CA;
DR   WPI; 97-043137/04.
DR   N-PSDB; T51371.
PT   DNA encoding human vascular endothelial growth factor 2 - used to
PT   promote angiogenesis or endothelialisation in vascular graft surgery
PS   Claim 1; Fig 2; 74pp; English.
CC   Human vascular endothelial growth factor 2 (VEGF2) (W11478) is
CC   structurally related to the VEGF/PDGF family and is a potent
CC   mitogen for vascular endothelial cells, stimulating their growth
CC   and angiogenesis.  The amino acid sequence of VEGF2 was deduced
CC   from a cDNA clone (T51371) obtd. from an early stage human (week 9)
CC   embryo cDNA library.  VEGF2 polypeptides can be produced in
CC   transformed host cells and used to promote angiogenesis e.g., to
CC   stimulate the growth of transplanted tissue following coronary
CC   bypass surgery, or to promote endothelialisation in vascular graft
CC   surgery.  It can also be used to screen for antagonists (useful
CC   e.g. for tumour therapy) and agonists of VEGF2 activity.
SQ   Sequence   419 AA;


  Query Match             36.0%;  Score 706.5;  DB 1;  Length 419;
  Best Local Similarity   38.9%;  Pred. No. 2.1e-49;
  Matches  140;  Conservative   61;  Mismatches   88;  Indels   71;  Gaps   11;

Qy      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
           |:|:|: ||::||: : : | ||:::|:||       :   :::||  :  : :|||  |
Db      57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114

Qy      95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
           : | || || ||::||| ||| |::|  | | :||||||||||:|:||||||| | | ||
Db     115 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174

Qy     155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
           ||||||:|| ||||:|||:  |: | :  |||| |:|:      |  :||||||:   :|
Db     175 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 234

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE---------ENPLAGTED----HSHLQE--- 255
           :  |  : | || : :|::: |:|: ||         ::   |  |    :  | |
Db     235 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291

Qy     255 ---------PALCGPH-----------------------MMFDEDRCECVCKTPCPKDL 281
                     || ||||                        |||: |:||||  ||::
Db     292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANRQFDENTCQCVCKRTCPRNQ 351

Qy     282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
             :|  |:| || || : |  | | ||  ||||      : ||| : : ||     : :|
Db     352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPCTNRQKACEPGFSYSEE 404


RESULT  12
W86237
ID   W86237 standard; protein; 399 AA.
AC   W86237;
DT   16-FEB-1999  (first entry)
DE   Human VEGF-C full length sequence.
KW   VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW   recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW   coronary; collateral vessel development; cell growth; migration; heart;
KW   lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW   wound healing; skin; vascular permeability.
OS   Homo sapiens.
PN   WO9849300-A2.
PD   05-NOV-1998.
PF   20-APR-1998; U07801.
PR   25-APR-1997; US-842984.
PA   (COLL-) COLLATERAL THERAPEUTICS.
PI   Bohlen P;
DR   WPI; 99-009426/01.
PT   New truncated vascular endothelial growth factor-related protein
PT   subunits - lack part of the N-terminal sequence, used to stimulate
PT   angiogenesis, e.g. for treating heart disease and ischaemia
PS   Claim 5; Fig 2D; 113pp; English.
CC   The invention relates to truncated VRP (vascular endothelial growth
CC   factor (VEGF)-related protein) subunits that have at least one amino acid
CC   N-terminal to the first Cys of the core sequence deleted. Host cells
CC   transformed or transfected with expression vectors containing nucleic
CC   acids encoding the truncated VRP subunits are used to produce the
CC   truncated proteins recombinantly. The truncated VRP subunits, optionally
CC   expressed from gene therapy vectors, have in vivo and in vitro angiogenic
CC   activity and are used to stimulate angiogenesis, particularly coronary
CC   collateral vessel development in cases of cardiac ischaemia; to stimulate
CC   endothelial cell growth and migration in vitro; to treat heart disease;
CC   to treat ischaemia (e.g.cardiac, chronic coronary or chronic lower limb
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CC   ischaemia; stroke and peripheral vascular disease); to promote healing of
CC   wounds (of skin or intestines), and to increase vascular permeability.
CC   Sequences W86234 to W86239 represent full length VRP sequences from
CC   which the truncated fragments are created.
SQ   Sequence   399 AA;


  Query Match             35.9%;  Score 704.5;  DB 1;  Length 399;
  Best Local Similarity   38.9%;  Pred. No. 2.9e-49;
  Matches  140;  Conservative   61;  Mismatches   88;  Indels   71;  Gaps   11;

Qy      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
           |:|:|: ||::||: : : | ||:::|:||       :   :::||  :  : :|||  |
Db      37 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 94

Qy      95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
           : | || || ||::||| ||| |::|  | | :||||||||||:|:|||||||| | | ||
Db      95 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 154

Qy     155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
           |||||||:|| ||||:|||:  |: | :  |||| |:|:      |  :||||||:   :|
Db     155 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 214

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE---------ENPLAGTED----HSHLQE--- 255
           :   |  : | || : :|::: |:|: ||         ::   |  |    :  | |
Db     215 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 271

Qy     255 ---------PALCGPH----------------------MMFDEDRCECVCKTPCPKDL 281
                  || ||||                        |||: |:|||| ||::
Db     272 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 331

Qy     282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
             :|  |:| || || : |  | | ||  ||||      : ||| : : ||     : :|
Db     332 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC------YRRPCTNRQKACEPGFSYSEE 384


RESULT  13
W00932
ID   W00932 standard; Protein; 419 AA.
AC   W00932;
DT   10-NOV-1997  (first entry)
DE   Human Flt4 receptor tyrosine kinase ligand VEGF-C.
KW   VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; human;
KW   vascular endothelial growth factor receptor-3; ligand;
KW   angiogenesis; wound healing; lymph vessel; lymphangioma;
KW   cancer; metastasis; therapy; diagnosis; antibody; inhibitor.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1. .102
FT                   /label= Prepro_peptide
FT   peptide         32. .227
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 15)"
FT   peptide         103. .217
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 12)"
FT   peptide         103. .225
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 13)"
FT   peptide         103. .227
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 14)"
FT   peptide         113. .213
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 10)"
FT   peptide         113. .227
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 11)"
FT   peptide         131. .211
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 9)"
FT   peptide         161. .221
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 8)"
PN   WO9705250-A2.
PD   13-FEB-1997.
PF   01-AUG-1996; FI0427.
PR   28-JUN-1996; US-671573.
PR   01-AUG-1995; US-510133.
PR   12-JAN-1996; US-585895.
PR   14-FEB-1996; US-601132.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI   Alitalo K,  Joukov V;
DR   WPI; 97-145688/13.
DR   N-PSDB; T84276.
PT   Flt4 receptor tyrosine kinase ligand and related nucleic acid - used
PT   to modulate growth of endothelial cells and for diagnosis of
PT   endothelial cell diseases
PS   Claim 7; Page 112-113; 183pp; English.
CC   This polypeptide comprises the pre-pro sequence of human VEGF-C,
CC   a novel ligand that binds specifically to human Flt4 receptor
CC   tyrosine kinase (VEGFR-3), stimulating phosphorylation of the
CC   receptor.  Its sequence was deduced from a cDNA clone (T84276)
CC   obtd. from a PC-3 prostatic adenocarcinoma cell (ATCC CRL 1435)
CC   library.  The polypeptide, or its active fragments, can be
CC   expressed in transformed or transfected host cells for use in
CC   claimed methods for detecting endothelial cells (e.g. to image
CC   lymphatic vessels, endothelial venules, Flt4 receptor in
CC   histochemical tissue) and also to modulate the growth of mammalian
CC   endothelial cells (e.g. to accelerate angiogenesis and to promote
CC   endothelial function of lymphatic vessels).  Inhibitors of
CC   VEGF-C, such as antibodies, can be used to control endothelial
CC   cell proliferation, e.g. lymphangioma or metastatic cancer.
CC   Mouse and quail VEGF-C sequences (see W00934-35) have also been
CC   isolated.
SQ   Sequence   419 AA;


  Query Match             35.9%;  Score 704.5;  DB 1;  Length 419;
  Best Local Similarity   38.9%;  Pred. No. 3e-49;
  Matches  140;  Conservative   61;  Mismatches   88;  Indels   71;  Gaps   11;

Qy      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
           |:|:|: ||::||: : : | ||:::|:||       :   :::||  :  : :|||  |
Db      57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114

Qy      95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
           : | || || ||::||| ||| |::|  | | :||||||||||:|:|||||||| | | ||
Db     115 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174

Qy     155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
           |||||||:|| ||||:|||:  |: | :  |||| |:|:      |  :||||||:   :|
Db     175 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 234

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE---------ENPLAGTED----HSHLQE--- 255
           :   |  : | || : :|::: |:|: ||         ::   |  |    :  | |
Db     235 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291

Qy     255 ---------PALCGPH----------------------MMFDEDRCECVCKTPCPKDL 281
                  || ||||                        |||: |:|||| ||::
Db     292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351

Qy     282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
             :|  |:| || || : |  | | ||  ||||      : ||| : : ||     : :|
Db     352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC------YRRPCTNRQKACEPGFSYSEE 404


RESULT  14
W17837
ID   W17837 standard; Protein; 419 AA.
AC   W17837;
DT   13-JAN-1998  (first entry)
DE   Human foetal liver kinase A binding protein flk-1bp.
KW   Foetal liver kinase 1 binding protein; human; flk-1bp;
KW   receptor tyrosine kinase; vasculogenesis; angiogenesis;
KW   wound healing; tumour; therapy; antagonist; antibody.
```

```
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= Sig_peptide
FT   Protein         21. .419
FT                   /label= Mat_protein
FT                   /note= "(Claim 10)"
FT   Peptide         21. .35
FT                   /label= N-terminal
FT                   /note= "(Claim 9)"
PN   WO9717442-A1.
PD   15-MAY-1997.
PF   05-NOV-1996; U17584.
PR   08-NOV-1995; US-554374.
PA   (IMMV ) IMMUNEX CORP.
PI   Lyman SD;
DR   WPI; 97-281031/25.
DR   N-PSDB; T68811.
PT   DNA encoding a human foetal liver kinase 1 binding protein  - used
PT   to treat conditions with insufficient protein, deliver agents to
PT   cells and identify antagonists to treat protein-mediated conditions
PS   Claim 1; Page 30-32; 43pp; English.
CC   This polypeptide comprises a human foetal liver kinase 1 binding
CC   protein (flk-1bp) (see W17837) that binds to the receptor tyrosine
CC   kinase flk-1 expressed on vascular endothelial and other cells.
CC   The mature flk1-bp can be secreted from host cells transformed with
CC   an expression vector including an isolated flk-1bp cDNA clone (see
CC   T68811).  Flk-1bp can be used to isolate cells to which it binds,
CC   for use in studying the roles of such cells and of flk-1 in
CC   vasculogenesis and angiogenesis.  Angiogenesis inhibition or
CC   increased vascularisation may be clinically desirable (e.g. to
CC   suppress solid tumour growth or in wound healing, respectively).
CC   The flk-1bp can be administered to treat conditions with defective
CC   or insufficient flk-1.  Polypeptides may also act as carriers to
CC   deliver diagnostic/therapeutic agents to cells to which flk1-bp
CC   binds, to generate antibodies, and to identify flk-1bp antagonists
CC   useful for treating flk-1bp mediated conditions.
SQ   Sequence   419 AA;

  Query Match             35.9%;  Score 704.5;  DB 1;  Length 419;
  Best Local Similarity   38.9%;  Pred. No. 3e-49;
  Matches  140;  Conservative   61;  Mismatches   88;  Indels   71;  Gaps   11;

Qy      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
           |:|:|: ||::||: : : | ||:::|:||       :   :::|| :  : :|||  |
Db      57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114

Qy      95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
           : | || || ||::||| ||| |::|  | | :||||||||||:|:|||||| | | ||
Db     115 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174

Qy     155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
           ||||||:|| ||||:|||:  |: | :  |||| |:|:      |  :||||||:   :|
Db     175 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 234

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE---------ENPLAGTED----HSHLQE--- 255
           :   |  : | || : :|::: |:|: ||         ::   |  |    :  | |
Db     235 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291

Qy     255 ---------PALCGPH----------------------MMFDEDRCECVCKTPCPKDL 281
                   || ||||                        |||: |:|||  ||::
Db     292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351

Qy     282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
             :|  |:| || || : |  | | ||  ||||      : ||| : : ||     : :|
Db     352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC------YRRPCTNRQKACEPGFSYSEE 404


RESULT  15
W75740
ID   W75740 standard; Protein; 419 AA.
AC   W75740;
DT   20-NOV-1998  (first entry)
DE   Human vascular endothelial growth factor C protein.
KW   Flt4; vascular endothelial growth factor C; vascular endothelial cell;
KW   lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation;
KW   lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
OS   Homo sapiens.
PN   WO9833917-A1.
PD   06-AUG-1998.
PF   02-FEB-1998; U01973.
PR   05-FEB-1997; US-795430.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
PI   Alitalo K, Joukov V;
DR   WPI; 98-437470/37.
DR   N-PSDB; V52576.
PT   New isolated vascular endothelial growth factor polypeptide(s) -
PT   used to develop products for treating, e.g. cancers, inflammation,
PT   oedema, granulocytopenia or for wound healing or tissue
PT   transplantation
PS   Claim 1; Page 112-115; 177pp; English.
CC   The vascular endothelial growth factor C (VEGF-C) polypeptides have
CC   activities affecting growth and migration of vascular endothelial cells,
CC   promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC   increasing vascular permeability, and affecting myelopoiesis.  The
CC   products can be used for stimulating angiogeneses, for inhibiting
CC   angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC   of inflammation, oedema, elephantiasis, or Milroy's disease.  They can
CC   also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC   They can also be used for modulating the growth of endothelial cells.
CC   They can also be used to stimulate lymphocyte production and maturation,
CC   and to promote or inhibit trafficking of leucocytes between tissues and
CC   lymphatic vessels or to affect migration in and out of the thymus.
SQ   Sequence   419 AA;

  Query Match             35.9%;  Score 704.5;  DB 1;  Length 419;
  Best Local Similarity   38.9%;  Pred. No. 3e-49;
  Matches  140;  Conservative   61;  Mismatches   88;  Indels   71;  Gaps   11;

Qy      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
           |:|:|: ||::||: : : | ||:::|:||       :   :::|| :  : :|||  |
Db      57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114

Qy      95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
           : | || || ||::||| ||| |::|  | | :||||||||||:|:|||||| | | ||
Db     115 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174

Qy     155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
           ||||||:|| ||||:|||:  |: | :  |||| |:|:      |  :||||||:   :|
Db     175 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 234

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE---------ENPLAGTED----HSHLQE--- 255
           :   |  : | || : :|::: |:|: ||         ::   |  |    :  | |
Db     235 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291

Qy     255 ---------PALCGPH----------------------MMFDEDRCECVCKTPCPKDL 281
                   || ||||                        |||: |:|||  ||::
Db     292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351

Qy     282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
             :|  |:| || || : |  | | ||  ||||      : ||| : : ||     : :|
Db     352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC------YRRPCTNRQKACEPGFSYSEE 404


Search completed: May 16, 2000, 15:27:04
Job time: 10484 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 16, 2000, 14:52:16 ; Search time 49.04 Seconds
(without alignments)
500.495 Million cell updates/sec

Title: US-09-214-982-1
Perfect score: 1963
Sequence: 1 MYREWVVVNVFMMLYVQLVQ.....HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1963	100.0	354	4	O43915	O43915 homo sapien
2	1675	85.3	358	11	P97946	P97946 mus musculu
3	1517.5	77.3	326	11	O35251	O35251 rattus norv
4	692	35.3	418	13	O57352	O57352 coturnix co
5	682.5	34.8	420	6	Q9XS50	Q9xs50 bos taurus
6	287	14.6	126	11	O35757	O35757 rattus norv
7	204	10.4	254	4	Q16889	Q16889 homo sapien
8	201	10.2	190	6	O77643	O77643 ovis aries
9	201	10.2	209	4	O60720	O60720 homo sapien
10	199	10.1	190	6	Q9XSF3	Q9xsf3 canis famil
11	198.5	10.1	194	13	O42572	O42572 xenopus lae
12	198.5	10.1	1704	5	Q94446	Q94446 chironomus
13	196	10.0	208	6	Q9XSF4	Q9xsf4 canis famil
14	195	9.9	191	4	O75875	O75875 homo sapien
15	191	9.7	214	6	Q9XSF5	Q9xsf5 canis famil
16	181.5	9.2	1698	5	Q94438	Q94438 chironomus
17	179.5	9.1	188	6	Q9XS48	Q9xs48 bos taurus
18	166.5	8.5	150	11	O54881	O54881 rattus norv
19	163.5	8.3	148	13	O42571	O42571 xenopus lae
20	163.5	8.3	188	13	O73682	O73682 brachydanio
21	163	8.3	132	12	Q9YMF3	Q9ymf3 orf virus.
22	161	8.2	149	6	Q9XS47	Q9xs47 bos taurus
23	161	8.2	210	6	Q29613	Q29613 felis silve
24	160.5	8.2	149	4	Q9Y6S8	Q9y6s8 homo sapien
25	158	8.0	158	11	Q63434	Q63434 rattus norv
26	156.5	8.0	141	11	O70123	O70123 mus musculu
27	155.5	7.9	110	11	O88911	O88911 rattus norv
28	147.5	7.5	207	11	Q64290	Q64290 mus musculu
29	147	7.5	193	6	Q9XS49	Q9xs49 bos taurus
30	146.5	7.5	207	4	Q16528	Q16528 homo sapien
31	142.5	7.3	144	13	O73822	O73822 brachydanio
32	139.5	7.1	1187	2	Q49549	Q49549 mycoplasma
33	139	7.1	68	6	O97500	O97500 oryctolagus
34	133	6.8	185	4	Q15354	Q15354 homo sapien
35	128	6.5	748	6	Q10741	Q10741 bos taurus
36	126	6.4	75	6	O18843	O18843 oryctolagus
37	125	6.4	704	3	O74567	O74567 trichoderma
38	125	6.4	2946	5	Q18857	Q18857 caenorhabdi
39	122.5	6.2	116	11	O35485	O35485 rattus norv
40	121.5	6.2	749	11	O35598	O35598 mus musculu
41	119.5	6.1	1106	5	Q9Y0Z5	Q9y0z5 drosophila
42	116.5	5.9	149	11	Q9WVQ7	Q9wvq7 mesocricetu
43	116	5.9	1548	11	Q62040	Q62040 mus musculu
44	115.5	5.9	1964	11	O35442	O35442 mus musculu
45	114.5	5.8	815	11	O88839	O88839 mus musculu

ALIGNMENTS

```
RESULT   1
O43915
ID   O43915      PRELIMINARY;      PRT;   354 AA.
AC   O43915;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GROWTH FACTOR FIGF.
GN   FIGF OR VEGF-D.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98140120.
RA   ROCCHIGIANI M., LESTINGI M., LUDDI A., ORLANDINI M., FRANCO B.,
RA   ROSSI E., BALLABIO A., ZUFFARDI O., OLIVIERO S.;
RT   "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT   between the PIGA and the GRPR genes.";
RL   Genomics 47:207-216(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RX   MEDLINE; 97349118.
RA   YAMADA Y., NEZU J., SHIMANE M., HIRATA Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98118549.
RA   ACHEN M.G., JELTSCH M., KUKK E., MAEKINEN T., VITALI A., WILKS A.F.,
RA   ALITALO K., STACKER S.A.;
RT   "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT   tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
DR   EMBL; Y12864; CAA73371.1; -.
DR   EMBL; Y12865; CAA73371.1; JOINED.
DR   EMBL; Y12866; CAA73371.1; JOINED.
DR   EMBL; Y12867; CAA73371.1; JOINED.
DR   EMBL; Y12868; CAA73371.1; JOINED.
DR   EMBL; Y12869; CAA73371.1; JOINED.
DR   EMBL; Y12870; CAA73371.1; JOINED.
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DR   EMBL; D89630; BAA24264.1; -.
DR   EMBL; AJ000185; CAA03942.1; -.
DR   EMBL; Y12863; CAA73370.1; -.
DR   HSSP; P15692; 1VPP.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
SQ   SEQUENCE   354 AA;  40444 MW;  310D8150 CRC32;


  Query Match             100.0%;  Score 1963;  DB 4;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-175;
  Matches  354;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60

Qy      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120

Qy     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180

Qy     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240

Qy     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC 300

Qy     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354


RESULT   2
P97946
ID   P97946      PRELIMINARY;      PRT;   358 AA.
AC   P97946;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR D (C-FOS INDUCED GROWTH FACTOR).
GN   VEGF-D OR FIGF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE; 97030254.
RA   ORDANDINI M., MARCONCINI L., FERRUZZI R., OLIVIERO S.;
RT   "Identification of a c-fos-induced gene that is related to the
RT   platelet-derived growth factor/vascular endothelial growth factor
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:11675-11675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RX   MEDLINE; 97349118.
RA   YAMADA Y., NEZU J., SHIMANE M., HIRATA Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
DR   EMBL; X99572; CAA67892.1; -.
DR   EMBL; D89628; BAA14002.1; -.
DR   HSSP; P15692; 1VPP.
DR   MGD; MGI:108037; Figf.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
SQ   SEQUENCE   358 AA;  40908 MW;  64E6B4E9 CRC32;


  Query Match             85.3%;  Score 1675;  DB 11;  Length 358;
  Best Local Similarity   83.8%;  Pred. No. 1.3e-148;
  Matches  301;  Conservative   20;  Mismatches   32;  Indels    6;  Gaps    2;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
           || ||  : |: || :| ||||  :|||||      |||:| ||||||||||||||||||:
Db       1 MYGEWGMGNILMMFHVYLVQGFRSEHGPVKDFSFERSSRSMLERSEQQIRAASSLEELLQ 60

Qy      56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           | |||||||||||:|||  ||||||||||||||||||| ||||||||||||||||||||
Db      61 IAHSEDWKLWRCRLKLKSLASMDSRSASHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE 120

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
           ||||||||||:|||||||||||||||||||| ::|||||||||||||||||||||||||||
Db     121 TCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEEGVMCMNTSTSYISKQLFEISVPLTSV 180

Qy     176 PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC 235
           |||||||:|||||||||| |||||||||||| |||| | ||||||||||||: ||||||||
Db     181 PELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC 240

Qy     236 VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKE 295
           |||:| || ||||||:|||| |||||| |||||||||||| ||| |||||||:||||||||
Db     241 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKAPCPGDLIQHPENCSCFECKE 300

Qy     296 SLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
           |||:||||||:|||||||||||||||||| ||| | || || ||||| | ||| :|:::||
Db     301 SLESCCQKHKIFHPDTCSCEDRCPFHTRTCASRKPACGKHWRFPKETR-AQGLYSQENP 358


RESULT   3
O35251
ID   O35251      PRELIMINARY;      PRT;   326 AA.
AC   O35251;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR D.
GN   VEGF-D.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE DAWLEY;
RX   MEDLINE; 97349118.
RA   YAMADA Y., NEZU J., SHIMANE M., HIRATA Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
DR   EMBL; AF014827; AAB66557.1; -.
DR   HSSP; P15692; 1VPP.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
SQ   SEQUENCE   326 AA;  37112 MW;  B30608D3 CRC32;


  Query Match             77.3%;  Score 1517.5;  DB 11;  Length 326;
  Best Local Similarity   85.2%;  Pred. No. 5.8e-134;
  Matches  270;  Conservative   20;  Mismatches   22;  Indels    5;  Gaps    1;

Qy       1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
           || ||  ||: || || |||| | ||  ||      |||:| ||||||||||||:||||:
Db       1 MYGEWAAVNILMMSYVYLVQGFSIEHRAVKDVSLERSSRSVLERSEQQIRAASTLEELLQ 60

Qy      56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           : ||||||||||||:|||  ::|||| |||||||||||| ||||||||||||||||||||
Db      61 VAHSEDWKLWRCRLKLKSLANVDSRSTSHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE 120

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
           ||||||||||:|||||||||||||||||||::|||||||||||||||||||||||||||||
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Db    121 TCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEESVMCMNTSTSYISKQLFEISVPLTSV 180

Qy    176 PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC 235
          |||||||:|||||||||||| |||||||||||||||||:| ||||||:|||||: ||||
Db    181 PELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQIPEEDQCPHSKKLCPVDMLWDNTKCKC 240

Qy    236 VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKE 295
          |||:|||| |||||||:|||||||||||||||||||||| ||| ||||||:|||||||||
Db    241 VLQDENPLPGTEDHSYLQEPALCGPHMMFDEDRCECVCKAPCPGDLIQHPENCSCFECKE 300

Qy    296 SLETCCQKHKLFHPDTC 312
          |||:||||||:||||||
Db    301 SLESCCQKHKMFHPDTC 317


RESULT   4
O57352
ID   O57352      PRELIMINARY;      PRT;   418 AA.
AC   O57352;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
GN   VEGF-C.
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98167900.
RA   EICHMANN A., CORBEL C., JAFFREDO T., BREANT V., JOUKOV V., KUMAR V.,
RA   ALITALO K., LE DOUARIN N.M.;
RT   "Avian VEGF-C: cloning, embryonic expression pattern and stimulation
RT   of the differentiation of VEGFR2-expressing endothelial cell
RT   precursors.";
RL   Development 125:743-752(1998).
DR   EMBL; Y15837; CAA75799.1; -.
DR   HSSP; P15692; 1VPP.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
KW   Signal.
FT   SIGNAL        1     31       POTENTIAL.
FT   CHAIN       111    418       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ   SEQUENCE   418 AA;  46839 MW;  B7862854 CRC32;


  Query Match             35.3%;  Score 692;  DB 13;  Length 418;
  Best Local Similarity   39.4%;  Pred. No. 7.6e-57;
  Matches  140;  Conservative   52;  Mismatches  101;  Indels   62;  Gaps    9;

Qy     41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
          |:|:|: ||::||: : : | ||:::|:||       :  :| |:||    | :||| |
Db     56 EEQLRSVSSVDELMTVLYPEYWKMFKCQLRKGGWQHNREHSSSDTRSDD--SLKFAAAHY 113

Qy     95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
          : | || || ||::||| ||| ||:|  | | :||||||||||:::|||||| | | ||
Db    114 NAEILKSIDTEWRKTQCMPREVCVDVGKEFGATTNTFFKPPCVSIYRCGGCCNSEGLQCM 173

Qy    155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSIQIPEE 212
          | ||:|||| ||||:|||:  |: | |  |||| |:|:      |  :||||||:    :
Db    174 NISTNYISKTLFEITVPLSHGPKPVTVSFANHTSCRCMSKLDVYRQVHSIIRRSLP-ATQ 232

Qy    213 DRCSHSKKLCPIDMLWDSNKCKCVLQEE---NPLAGTED---------------------- 249
          :|  : | || : :|::  |:|: | :   :   |  |
Db    233 TQCHVANKTCPKNHVWNNQICRCLAQHDFGFSSHLGDSDTSEGFHICGPNKELDEETCQC 292

Qy    249 -------------HSHLQE------------PALCGPHMMFDEDRCECVCKTPCPKDLIQ 283
                       |  |                |: |||:  |||::|:|||| |||
Db    293 VCKGGVRPISCGPHKELDRASCQCMCKNKLLPSSCGPNKEFDEEKCQCVCKKTCPKHHPL 352

Qy    284 HPKNCSCFECKESLETCCQKHKLFHPDTCSC-EDRCPFHTRPCASGKTACAKHCR 337
          :|  | | || ||   |  | | ||  ||||    |   |: | :|     : ||

Db    353 NPAKCIC-ECTESPNKCFLKGKRFHHQTCSCYRPPCTVRTKRCDAGFLLAEEVCR 406


RESULT   5
Q9XS50
ID   Q9XS50      PRELIMINARY;      PRT;   420 AA.
AC   Q9XS50;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   LIU X., YONEKURA H., YAMAGISHI S., YAMAMOTO Y., YAMAMOTO H.;
RT   "Structure and expression of bovine VEGF family.";
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB004275; BAA77687.1; -.
DR   PROSITE; PS00249; PDGF; 1.
KW   Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    420       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ   SEQUENCE   420 AA;  46681 MW;  918E357F CRC32;


  Query Match             34.8%;  Score 682.5;  DB 6;  Length 420;
  Best Local Similarity   37.7%;  Pred. No. 5.9e-56;
  Matches  133;  Conservative   60;  Mismatches   89;  Indels   71;  Gaps   10;

Qy     41 EQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRST----RFAATFYDI 96
          |:|:|: ||::||: : : | ||:::|:||   :     :: ::  |    :|||  |:
Db     58 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHSTEQANTNIRTGETLKFAAAHYNT 117

Qy     97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
          | |: || ||::||| ||| |::|  | | :||||||||||:|:|||||| |   ||||
Db    118 EILRSIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCCNSEGQQCMNT 177

Qy    157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIPEE 212
          ||||:|| ||||:|||:  |: | :  |||| |:|:      |  :||||||:   :|:
Db    178 STSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPAALPQ- 237

Qy    213 DRCSHSKKLCPIDMLWDSNKCKCVLQEE---NPLAGTED---------------------- 249
            |  : | || | :|::: |:|: | :   :| || :
Db    237 --CQAANKTCPADYIWNNHVCRCLAQHDFIFSPSAGDDSADGFHDICGPNKELDEETCQC 294

Qy    249 -------------HSHLQE------------PALCGPHMMFDEDRCECVCKTPCPKDLIQ 283
                       |  |                |: || :  |||: |:|:||  ||::
Db    295 VCKGGLQASSCGPHKELDRDSCQCVCKNKLFPSSCGANREFDENTCQCICKKTCPRNQPL 354

Qy    284 HPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHC 336
          :|  |:| || |: : |  | | |   ||||      : |||    |   |||
Db    355 NPGKCAC-ECTENPQKCFLKGKKFQHQTCSC------YRRPC----TNRVKHC 396


RESULT   6
O35757
ID   O35757      PRELIMINARY;      PRT;   126 AA.
AC   O35757;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR-C (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=LUNG;
RA   MANDRIOTA S.J., PEPPER M.S.;
```

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RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF010302; AAB63248.1; -.
DR   HSSP; P15692; 2VPF.
FT   NON_TER       1      1
FT   NON_TER     126    126
SQ   SEQUENCE   126 AA;  13977 MW;  DC008358 CRC32;


  Query Match             14.6%;  Score 287;  DB 11;  Length 126;
  Best Local Similarity   44.2%;  Pred. No. 1.3e-19;
  Matches   57;  Conservative   24;  Mismatches   40;  Indels    8;  Gaps    4;

Qy     137 VNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP 196
           |:|:||||||| | | |||||| |:|| ||||:|||:  |: | :  |||| |:|:
Db       1 VSVYRCGGCCNSEGLQCMNTSTGYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLD 60

Qy     197 --RHPYSIIRRSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPL-AGTEDHSH 251
             |  :|||||:   :|:   |  : | || : :|::  |:|: |::    :  || |
Db      61 VYRQVHSIIRRSLPATLPQ---CQAANKTCPANYVWNNYMCQCLAQQDFIFYSNVEDDSS 117

Qy     252 LQEPALCGP 260
           :|||
Db     118 NGFHDVCGP 126


RESULT   7
Q16889
ID   Q16889      PRELIMINARY;      PRT;   254 AA.
AC   Q16889;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
GN   VEGF 206.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92168017.
RA   HOUCK K.A., FERRARA N., WINER J., CACHIANES G., LI B., LEUNG D.W.;
RT   "The vascular endothelial growth factor family: identification of a
RT   fourth molecular species and characterization of alternative splicing
RT   of RNA.";
RL   Mol. Endocrinol. 5:1806-1814(1991).
DR   EMBL; S85192; AAC63102.1; -.
DR   EMBL; S85224; AAC63101.1; -.
DR   EMBL; S85199; AAC63101.1; JOINED.
DR   EMBL; S85201; AAC63101.1; JOINED.
DR   EMBL; S85219; AAC63101.1; JOINED.
DR   EMBL; S85222; AAC63101.1; JOINED.
DR   HSSP; P15692; 2VPF.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   254 AA;  29461 MW;  DC203C10 CRC32;


  Query Match             10.4%;  Score 204;  DB 4;  Length 254;
  Best Local Similarity   23.6%;  Pred. No. 1.5e-11;
  Matches   70;  Conservative   31;  Mismatches  106;  Indels   90;  Gaps   11;

Qy      45 RAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSA--------SHRSTRFAATFYDI 96
           ||: ::  ||      |  |   | |    :  |::|        :|
Db      18 RASETMNFLL------SWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHH---------- 61

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : ||||||:| | |: |
Db      61 EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 119

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
           | |: |:  |       |     :  :    |  |:|                    |::
Db     120 EESNITMQIMRIK------PHQGQHIGEMSFLQHNKCECR----------------PKK 156

Qy     213 DRCSHSKKLCPIDMLWDSNK-------------CKCVLQEENPLAGTEDHSHLQEPALC 258
           ||    ||           |               :| |   :         |  | |
Db     157 DRARQEKKSVRGKGKGQKRKRKKSRYKSWSVYVGARCCLMPWS----------LPGPHPC 206

Qy     259 GPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           ||          |         :| |: | |  || :   | :     :  || |:
Db     207 GP-----------CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 250


RESULT   8
O77643
ID   O77643      PRELIMINARY;      PRT;   190 AA.
AC   O77643;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR.
GN   VEGF.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Caprinae; Ovis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA-RAMBOULLIET;
RA   CHEUNG C.Y., BRACE R.A.;
RT   "Ovine vascular endothelial growth factor: Nucleotide sequence and
RT   expression in fetal tissues.";
RL   Growth Factors 0:0-0(1998).
DR   EMBL; AF071015; AAC23608.1; -.
DR   HSSP; P15692; 2VGH.
DR   PROSITE; PS00249; PDGF; 1.
DR   PFAM; PF00341; PDGF; 1.
SQ   SEQUENCE   190 AA;  22342 MW;  ACAF3FAF CRC32;


  Query Match             10.2%;  Score 201;  DB 6;  Length 190;
  Best Local Similarity   25.4%;  Pred. No. 2.1e-11;
  Matches   57;  Conservative   21;  Mismatches   66;  Indels   80;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:||| |: |
Db      38 EVMKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
           |: |:  |                                |    :|          | |
Db      97 EEFNITMQIMRIK----------------------PHQSQH----------IGEMSFLQ 123

Qy     217 HSKKLCPIDMLWDSNKCKC-----VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC 271
           |              |||:|       ::|||          |||
Db     124 H------------NKCECRPKKDKARQENP--------------CGP---------- 145

Qy     272 VCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |         :| |: | |  || :   |  :    :  || |:
Db     145 -CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   9
O60720
ID   O60720      PRELIMINARY;      PRT;   209 AA.
AC   O60720;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   VEGF183 PROTEIN PRECURSOR (VASCULAR ENDOTHELIAL GROWTH FACTOR 183).
GN   VEGF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 16, 2000, 14:35:17 ; Search time 48.21 Seconds
(without alignments)
430.511 Million cell updates/sec

Title: US-09-214-982-1
Perfect score: 1963
Sequence: 1 MYREWVVVNVFMMLYVQLVQ.....HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	704.5	35.9	419	2	S69207	vascular endotheli
2	200.5	10.2	232	2	A41551	vascular endotheli
3	200	10.2	190	2	B40080	vascular endotheli
4	198	10.1	190	2	S52130	vascular endotheli
5	198	10.1	190	2	B44881	vascular endotheli
6	198	10.1	214	2	A44881	vascular endotheli
7	194	9.9	190	2	A35987	glioma-derived vas
8	181.5	9.2	1700	2	S08167	Balbiani ring 3 pr
9	176.5	9.0	188	2	JC4680	vascular endotheli
10	167.5	8.5	146	2	S57956	ovine vascular end
11	166.5	8.5	120	2	A33787	vascular endotheli
12	164	8.4	148	2	D49530	16K vascular endot
13	161	8.2	245	1	TVCTSS	platelet-derived g
14	160.5	8.2	149	2	A41236	placental growth f
15	158	8.0	158	2	A56125	placental growth f
16	147.5	7.5	207	2	JC4679	vascular endotheli
17	145	7.4	133	2	B49530	vascular endotheli
18	145	7.4	241	1	PFHUG2	platelet-derived g
19	139.5	7.1	1187	2	T18355	hypothetical prote
20	135	6.9	230	2	A55030	platelet-derived g
21	135	6.9	241	1	PFMSGB	platelet-derived g
22	133.5	6.8	225	2	S25097	platelet-derived g
23	133	6.8	185	2	S58383	hypothetical prote
24	128	6.5	748	2	S66129	disintegrin (EC 3.
25	126	6.4	161	2	I38108	platelet-derived g
26	125.5	6.4	196	2	B28964	platelet-derived g
27	125.5	6.4	211	1	PFHUG1	platelet-derived g
28	125	6.4	2946	2	T15840	hypothetical prote
29	122	6.2	226	1	TVMVSS	PDGF-related trans
30	120.5	6.1	160	2	JQ0542	185K secretory pro
31	120	6.1	200	2	I51551	platelet-derived g
32	120	6.1	215	2	S08220	platelet-derived g
33	120	6.1	226	2	I51550	platelet-derived g
34	118	6.0	965	2	S62935	hypothetical prote
35	116	5.9	1548	2	S34583	serine proteinase
36	115.5	5.9	1964	2	T09059	notch4 - mouse
37	114.5	5.8	1287	2	A41685	SIL protein - huma
38	114.5	5.8	5376	2	T42215	zonadhesin - mouse
39	113	5.8	197	2	S25096	platelet-derived g
40	113	5.8	846	2	A30889	integrin beta chai
41	112.5	5.7	2195	2	T34264	hypothetical prote
42	112	5.7	3635	2	T10053	laminin alpha 5 ch
43	111.5	5.7	336	2	D69074	polyferredoxin 4x2
44	111.5	5.7	2219	2	T27684	hypothetical prote
45	111	5.7	198	2	JS0735	platelet-derived g

ALIGNMENTS

RESULT 1
S69207
vascular endothelial growth factor C precursor - human
N;Alternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C;Accession: S69207; S61795; S71443; S69208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A;Reference number: S69207; MUID:96203094
A;Accession: S69207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-419 <JOU>
A;Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g118
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4
A;Reference number: S61795; MUID:96178224
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 70-419 <JOU1>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

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  Query Match           35.9%;  Score 704.5;  DB 2;  Length 419;
  Best Local Similarity 38.9%;  Pred. No. 1.9e-45;
  Matches  140;  Conservative   61;  Mismatches   88;  Indels   71;  Gaps   11;

Qy      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFY 94
           |:|:|: ||::||: : : | ||:::|:||       :   :::|| :  : :|||  |
Db      57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114

Qy      95 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
           : | || || ||::||| ||| |::|  | | :||||||||||:|:|||||| | | ||
Db     115 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174

Qy     155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
           |||||:|| ||||:|||:  |: | :  |||| |:|:      |  :|||||:   :|
Db     175 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 234

Qy     211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE---------ENPLAGTED----HSHLQE--- 255
           :   |  : | || : :|::: |:|: ||          ::   |  |    :  | |
Db     235 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291

Qy     255 ---------PALCGPH----------------------MMFDEDRCECVCKTPCPKDL 281
                   || ||||                      |||: |:|||| ||::
Db     292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351

Qy     282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
           :|  |:| || || : |  | | ||  ||||      : ||| : : ||     : :|
Db     352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC------YRRPCTNRQKACEPGFSYSEE 404
```

RESULT 2
A41551
vascular endothelial growth factor 206 precursor - human
N;Alternate names: vascular permeability factor
N;Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VEGF
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C;Accession: A41551; C41551; B41551; A40454; B40454; C40454; A40079; A40080; JQ1463; JQ1
R;Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.
Mol. Endocrinol. 5, 1806-1814, 1991
A;Title: The vascular endothelial growth factor family: identification of a fourth molec
A;Reference number: A41551; MUID:92168017
A;Accession: A41551
A;Molecule type: mRNA
A;Residues: 1-232 <HOU1>
A;Cross-references: GB:S85192; NID:g246155; PID:g246156
A;Accession: C41551
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-140,'N',183-232 <HOU2>
A;Accession: B41551
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-141,227-232 <HOU>
R;Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.; Ab
J. Biol. Chem. 266, 11947-11954, 1991
A;Title: The human gene for vascular endothelial growth factor. Multiple protein forms a
A;Reference number: A40454; MUID:91268072
A;Accession: A40454
A;Molecule type: DNA
A;Residues: 1-165,183-232 <TI1>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976; GE
A;Accession: B40454
A;Molecule type: DNA
A;Residues: 1-140,'N',183-232 <TI2>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977; GE
A;Accession: C40454
A;Molecule type: DNA
A;Residues: 1-141,227-232 <TI3>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978
R;Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.T.
Science 246, 1309-1312, 1989
A;Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A;Reference number: A40079; MUID:90069609
A;Accession: A40079
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-165,183-232 <KEC>
A;Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301
R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A;Reference number: A40080; MUID:90069608
A;Accession: A40080
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140,'N',183-232 <LEU>
A;Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971
R;Weindel, K.; Marme, D.; Weich, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A;Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endotheli
A;Reference number: JQ1463; MUID:92231879
A;Accession: JQ1463
A;Molecule type: mRNA
A;Residues: 1-140,'N',183-232 <WEI>
A;Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659
A;Experimental source: AIDS-Kaposi's sarcoma cell
A;Accession: JQ1464
A;Molecule type: mRNA
A;Residues: 1-140,'N',227-232 <WE2>
A;Experimental source: AIDS-Kaposi's sarcoma cell
R;Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.;
J. Biol. Chem. 264, 20017-20024, 1989
A;Title: Human vascular permeability factor. Isolation from U937 cells.
A;Reference number: A34492; MUID:90062112
A;Accession: A34492
A;Molecule type: protein
A;Residues: 27-36;43-49,'R';72-76,'Q',78-81;59-71 <CON>
C;Comment: The most common of several alternatively spliced forms is VEGF 165.
C;Genetics:
A;Gene: GDB:VEGF
A;Cross-references: GDB:132244; OMIM:192240
A;Map position: 6p21-6p12
C;Function:
A;Description: promotes fluid and protein leakage from blood vessels
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular
F;1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <
F;1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status pre
F;1-141,227-232/Product: vascular endothelial growth factor 121 precursor #status pre
F;1-26/Domain: signal sequence #status predicted <SIG>
F;101/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
  Query Match           10.2%;  Score 200.5;  DB 2;  Length 232;
  Best Local Similarity 24.9%;  Pred. No. 4e-08;
  Matches   59;  Conservative   24;  Mismatches   89;  Indels   65;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |         ||| || : |||||||:| | |: |
Db      39 EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 97

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
             | |: |:  |       |      :  :    |  |:|                  |::
Db      98 EESNITMQIMRIK------PHQGQHIGEMSFLQHNKCECR-----------------PKK 134

Qy     213 DRCSHSKKLCPIDMLWDSNK-------------CKCVLQEENPLAGTEDHSHLQEPALC 258
           ||    ||           |                :| |   :          | | |
Db     135 DRARQEKKSVRGKGKGQKRKRKKSRYKSWSVYVGARCCLMPWS----------LPGPHPC 184

Qy     259 GPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           ||           |          :| |: | |  || :   |  :    :  || |:
Db     185 GP------------CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 228
```

RESULT 3

```
B40080
vascular endothelial growth factor precursor (version 2) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C;Accession: B40080; B33787; A33255
R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A;Reference number: A40080; MUID:90069608
A;Accession: B40080
A;Molecule type: mRNA
A;Residues: 1-190 <LEU>
A;Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007
R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
A;Reference number: A33787; MUID:90121225
A;Accession: B33787
A;Molecule type: mRNA
A;Residues: 27-190 <TIS>
A;Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
R;Ferrara, N.; Henzel, W.J.
Biochem. Biophys. Res. Commun. 161, 851-858, 1989
A;Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specif
A;Reference number: A33255; MUID:89286596
A;Accession: A33255
A;Molecule type: protein
A;Residues: 27-31 <FER>
C;Keywords: alternative splicing; glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-190/Product: vascular endothelial growth factor #status predicted <MAT>
F;100/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            10.2%;  Score 200;  DB 2;  Length 190;
  Best Local Similarity   25.4%;  Pred. No. 3.6e-08;
  Matches   57;  Conservative   21;  Mismatches   66;  Indels   80;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:|||  |: |
Db      38 EVVKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
               |: |:  |                        |   :|          | |
Db      97 EEFNITMQIMRIK----------------------PHQSQH----------IGEMSFLQ 123

Qy     217 HSKKLCPIDMLWDSNKCKC-----VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC 271
           |             |||:|       ::|||                 |||
Db     124 H-------------NKCECRPKKDKARQENP--------------CGP---------- 145

Qy     272 VCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |         :| |: | |  || :   |  :    :  || |:
Db     145 -CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   4
S52130
vascular endothelial growth factor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S52130
R;Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the porcine vascular endothelial growth f
A;Reference number: S52130; MUID:95143284
A;Accession: S52130
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <SHA>
A;Cross-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

  Query Match            10.1%;  Score 198;  DB 2;  Length 190;
  Best Local Similarity   24.2%;  Pred. No. 5.1e-08;
  Matches   54;  Conservative   24;  Mismatches   67;  Indels   78;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |        ||| || : |||||||:| | |: |
Db      38 EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 96

Qy     157 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
               |: |:  |       |     :  :    |  |:|                   |::
Db      97 EEFNITMQIMRIK------PHQGQHIGEMSFLQHNKCECR----------------PKK 133

Qy     213 DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
           ||                          ::|||              |||
Db     134 DRA----------------------RQENP--------------CGP------------ 145

Qy     273 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           |         :| |: | |  || :   |  :    :  || |:
Db     145 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   5
B44881
vascular endothelial growth factor-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C;Accession: B44881; A43351; A61029
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenes
A;Reference number: A44881; MUID:92274860
A;Accession: B44881
A;Molecule type: mRNA
A;Residues: 1-190 <BRE>
A;Cross-references: GB:S38083; NID:g249858; PIDN:AAB22253.1; PID:g249859
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)
R;Claffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A;Title: Vascular endothelial growth factor. Regulation by cell differentiation and a
A;Reference number: A43351; MUID:92355593
A;Accession: A43351
A;Molecule type: mRNA
A;Residues: 1-116,'ER',119-190 <CLA>
A;Cross-references: GB:M95200; NID:g202350; PIDN:AAA40547.1; PID:g202351
A;Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBIP:110675)
R;Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A;Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelia
A;Reference number: A61029; MUID:91197543
A;Accession: A61029
A;Molecule type: protein
A;Residues: 27-38 <ROS>
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein;

  Query Match            10.1%;  Score 198;  DB 2;  Length 190;
  Best Local Similarity   22.6%;  Pred. No. 5.1e-08;
  Matches   60;  Conservative   30;  Mismatches   78;  Indels   98;  Gaps   10;

Qy      62 WKLWRCRLRL--------KSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113
           |  |   | |        ::  : :    ||            | :| :|  :||: | |
Db       7 WVHWTLALLLYLHHAKWSQAAPTTEGEQKSH-----------EVIKFMD-VYQRSYCRP 53

Qy     114 RETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLT 173
            || |::  |        ||| || : || ||||:|:| |: || | |: |:  |  |
Db      54 IETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPTSESNITMQIMRIK-PHQ 112

Qy     174 SVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKC 233
           |   :  :   |: |:|              |::||
Db     113 S-QHIGEMSFLQHSRCECR----------------PKKDRTK---------------- 138

Qy     234 KCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKD----LIQHPKNCS 289
                                          |: ||    || :     :| |: |
```

```
Db    138 ------------------------------PENHCE-----PCSERRKHLFVQDPQTCK 161

Qy    290 CFECKESLETCCQKHKLFHPDTCSCE 315
          |  || :   |   :     :  || |:
Db    162 C-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   6
A44881
vascular endothelial growth factor-3 precursor - mouse
N;Contains: vascular endothelial growth factor-2; vascular permeability factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: A44881; C44881; A60932; S52136
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A;Reference number: A44881; MUID:92274860
A;Accession: A44881
A;Molecule type: mRNA
A;Residues: 1-214 <BRE>
A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22252.1; PID:g249857
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIP:104678)
A;Accession: C44881
A;Molecule type: mRNA
A;Residues: 1-140,209-214 <BR2>
A;Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1; PID:g249861
A;Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIP:107625)
R;Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothel
A;Reference number: A60932; MUID:91079755
A;Accession: A60932
A;Molecule type: protein
A;Residues: 27-33 <CLA>
R;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1224, 365-370, 1994
A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous im
A;Reference number: S52136; MUID:95101726
A;Accession: S52136
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-46 <SUG>
C;Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C;Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodimer;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>

  Query Match              10.1%;  Score 198;  DB 2;  Length 214;
  Best Local Similarity    23.7%;  Pred. No. 5.7e-08;
  Matches   63;  Conservative   35;  Mismatches   94;  Indels   74;  Gaps   11;

Qy      62 WKLWRCRLRL--------KSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113
           |   |   | |        ::  :  :    ||           | :| :|  :||: | |
Db       7 WVHWTLALLLYLHHAKWSQAAPTTEGEQKSH-----------EVIKFMD-VYQRSYCRP 53

Qy     114 RETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLT 173
           || |::  |        ||| || : || ||||:|:| |: || | |: |:  |  |
Db      54 IETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPTSESNITMQIMRIK-PHQ 112

Qy     174 SVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKC 233
           |   :  :    |: |:|                |::||    ||      :    |
Db     113 S-QHIGEMSFLQHSRCECR----------------|::||    ||      :    |
Qy     234 KCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKD----LIQHPKNCS 289
           :  ::::       |                  ||     || :      :| |: |
Db     150 QKRKRKKSRFKSWSVH----------------CE-----PCSERRKHLFVQDPQTCK 185
Qy     290 CFECKESLETCCQKHKLFHPDTCSCE 315
           |  || :   |   :     :  || |:
Db     186 C-SCKNTDSRCKARQLELNERTCRCD 210


RESULT   7
A35987
glioma-derived vascular endothelial cell growth factor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C;Accession: A35987
R;Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Ho
Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is
A;Reference number: A35987; MUID:90207249
A;Accession: A35987
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <CON>
A;Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288

  Query Match               9.9%;  Score 194;  DB 2;  Length 190;
  Best Local Similarity    23.8%;  Pred. No. 1e-07;
  Matches   53;  Conservative   27;  Mismatches   65;  Indels   78;  Gaps    8;

Qy      97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
           | :| :|  :||: | | || |::  |         ||| || : || ||||:|:| |: |
Db      38 EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPT 96

Qy     157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
           | | :: |:  |  |  |   :  :    |: |:|                  |::||
Db      97 SESNVTMQIMRIK-PHQS-QHIGEMSFLQHSRCECR----------------|::||
Qy     217 HSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTP 276
                                                              |: ||     |
Db     138 ------------------------------------------------PENHCE-----P 144
Qy     277 CPKD----LIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
           | :      :| |: | |  || :   |  :     :  || |:
Db     145 CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 186


RESULT   8
S08167
Balbiani ring 3 protein - midge (Chironomus tentans)
C;Species: Chironomus tentans
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Mar-1998
C;Accession: S08167
R;Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A;Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive str
A;Reference number: S08167; MUID:90172404
A;Accession: S08167
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1700 <PAU>
A;Cross-references: GB:X52263; NID:g7057; PID:g7058
C;Genetics:
A;Gene: BR3
A;Map position: 4

  Query Match               9.2%;  Score 181.5;  DB 2;  Length 1700;
  Best Local Similarity    19.9%;  Pred. No. 6.8e-06;
  Matches   68;  Conservative   43;  Mismatches  105;  Indels  125;  Gaps   15;

Qy     109 TQCSPRETCVEVASELGKSTNTFFKPPCVNVFR-----CGGCCNEESLICMNTSTSYISK 163
           |:|| ::  :|  | |  | |          | : ||     ||  |:::   |        |
Db    1073 TKCSDKQKFIESKCECGCETQT----QCKDGFRWSNLECGCLCDDKK--CP-------GK 1119
Qy     164 QLFEISVPLTSVPELVPVKVANH--------TGCKCLPTAPRHPYSIIRR------SIQI 209
           |:|: :      |   |     :                |||    | :  : ::      :
Db    1120 QVFDKNTCQCKCPNQKPGDTCGNGKDFCPLDCSCKCKNPKPANGCTGVQEWNEEKCQCEC 1179
Qy     210 PEE------------------------DRCSHSKKL----------------CPIDML 227
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          |::                              ||:::|                    || : :
Db   1180 PKDKPKKQCPGGQDWNNHQCQCGCPTPAPTCSNNQKYSNVSCSCGCNPGKPKNGCPGNQI 1239

Qy    228 WDSNKCKCVLQE--ENP-----------------------------------LAGTEDH 249
          |  | |:||  :  | |                                     |
Db   1240 WCDNTCRCVCPKNMEKPADNCKTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECP 1299

Qy    250 SHLQEPALCGPHMMFDEDRCECVCKTP-----CPKDLIQHPKNCSCFECKESLETCCQKH 304
          :   :|| ||    :::| | | ||:      || :   : |:|   ||| |    |
Db   1300 ADKAKPASCGDKKSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDC---ECKCSATGNCPAG 1356

Qy    305 KLFHPDTCSCEDRCPFHTRPCASGKTACAKHCR--FPKEKR 343
          : ::  || |   ||  |  |   :  |:| |:   | :|:
Db   1357 QTWNSQTCQCS--CP-ATGKCTGAQVWCSKACKCVCPAQKK 1394


RESULT   9
JC4680
vascular endothelial growth factor-related factor 167 precursor - mouse
N;Alternate names: VRF 167 protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C;Accession: JC4680
R;Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjoeld, M.; Weber, G.;
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A;Title: Characterization of the murine VEGF-related factor gene.
A;Reference number: JC4679; MUID:96183052
A;Accession: JC4680
A;Molecule type: mRNA
A;Residues: 1-188 <TOW>
A;Cross-references: GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g1314336
C;Comment: This factor is a mitogen, that is selective for endothelial cells, and belong
ar endothelial growth factors 167 and VEGF 186.
C;Genetics:
A;Gene: vrf
A;Map position: 19
A;Introns: 137/2
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-188/Product: vascular endothelial growth factor-related factor #status predicted <M


  Query Match             9.0%;  Score 176.5;  DB 2;  Length 188;
  Best Local Similarity   23.3%;  Pred. No. 2e-06;
  Matches   49;  Conservative   22;  Mismatches   70;  Indels   69;  Gaps    7;

Qy    106 WQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQL 165
          : |  | |||  | :: ||  :      | || | |||||| :: | |: |    :  |:
Db     42 YARATCQPREVVVPLSMELMGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQI 101

Qy    166 FEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPID 225
            |  | : : |:    :  |: |:| |          : |   |:  |      |||
Db    102 LMIQYPSSQLGEM---SLEEHSQCECRPKK--------KESAVKPDSPRI-----LCP-- 144

Qy    226 MLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHP 285
                  |  : : |                                          |
Db    144 --------PCTQRRQRP-----------------------------------------DP 154

Qy    286 KNCSCFECKESLETCCQKHKL-FHPDTCSC 314
          : | |  |:      ||   |  :|||| |
Db    155 RTCRC-RCRRRRFLHCQGRGLELNPDTCRC 183


RESULT  10
S57956
ovine vascular endothelial growth factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S57956
R;Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.
submitted to the EMBL Data Library, July 1995
A;Reference number: S57956
A;Accession: S57956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <RED>
A;Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351


  Query Match             8.5%;  Score 167.5;  DB 2;  Length 146;
  Best Local Similarity   38.1%;  Pred. No. 7.5e-06;
  Matches   37;  Conservative   14;  Mismatches   43;  Indels    3;  Gaps    3;

Qy     97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
          | :| :|  :||: | | || |::  |        ||| || : |||||||:||| |: |
Db     38 EVMKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 96

Qy    157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLP 193
             |: |:  |  |  |   :  :    |  |:| |
Db     97 EEFNITMQIMRIK-PHQS-QHIGEMSFLQHNKCECRP 131


RESULT  11
A33787
vascular endothelial growth factor (version 1) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999
C;Accession: A33787
R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Cr
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet-derived gro
A;Reference number: A33787; MUID:90121225
A;Accession: A33787
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <TIS>
A;Cross-references: GB:M33750; NID:g163810; PIDN:AAA30805.1; PID:g163811
C;Keywords: alternative splicing


  Query Match             8.5%;  Score 166.5;  DB 2;  Length 120;
  Best Local Similarity   38.1%;  Pred. No. 7.4e-06;
  Matches   37;  Conservative   14;  Mismatches   43;  Indels    3;  Gaps    3;

Qy     97 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
          | :| :|  :||: | | || |::  |        ||| || : |||||||:||| |: |
Db     12 EVVKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 70

Qy    157 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLP 193
             |: |:  |  |  |   :  :    |  |:| |
Db     71 EEFNITMQIMRIK-PHQS-QHIGEMSFLQHNKCECRP 105


RESULT  12
D49530
16K vascular endothelial growth factor homolog A2R - Orf virus
C;Species: Orf virus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: D49530
R;Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o
A;Reference number: A49530; MUID:94076465
A;Contents: NZ7
A;Accession: D49530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <LYT>
A;Cross-references: GB:S67522; NID:g456900; PIDN:AAB29223.1; PID:g456902
A;Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIP:141426)


  Query Match             8.4%;  Score 164;  DB 2;  Length 148;
  Best Local Similarity   32.8%;  Pred. No. 1.4e-05;
  Matches   38;  Conservative   12;  Mismatches   40;  Indels   26;  Gaps    4;

Qy    105 EWQRT----QCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSY 160
```

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          :| ||     | ||:| | :  |  :|||  : | || | || |||| :  ||    |
Db      36 DWMRTLDKSGCKPRDTVVYLGEEYPESTNLQYNPRCVTVKRCSGCCNGDGQICTAVETRN 95

Qy     161 ISKQLFEISVPLTSV----------PELVPVKVANHTGCKCL------PTAPRHP 199
           :     ::| :| |            |  : |  || | |:      ||  | |
Db      96 TT-----VTVSVTGVSSSSGTNSGVSTNLQRISVTEHTKCDCIGRTTTPTTTREP 146


RESULT  13
TVCTSS
platelet-derived growth factor chain B precursor - cat
N;Alternate names: PDGF-related transforming protein
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Mar-1996
C;Accession: A26402
R;Van den Ouweland, A.M.W.; Van Groningen, J.J.M.; Schalken, J.A.; Van Neck, H.W.; Bloem
Nucleic Acids Res. 15, 959-970, 1987
A;Title: Genetic organization of the c-sis transcription unit.
A;Reference number: A26402; MUID:87146463
A;Accession: A26402
A;Molecule type: mRNA
A;Residues: 1-245 <VAN>
C;Genetics:
A;Gene: sis
C;Superfamily: platelet-derived growth factor
C;Keywords: glycoprotein; growth factor; platelet; proto-oncogene; transforming protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-81/Domain: propeptide #status predicted <PRO>
F;82-194/Product: platelet-derived growth factor chain B #status predicted <MAT>
F;163-167/Region: receptor binding #status predicted
F;63/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             8.2%;  Score 161;  DB 1;  Length 245;
  Best Local Similarity   29.9%;  Pred. No. 3.7e-05;
  Matches   67;  Conservative   24;  Mismatches  103;  Indels   30;  Gaps   10;

Qy       1 MYREWVVVNVFMML--YVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITH 58
           | | |    :|: |  |::||   | |  |:      |  |:  ||   | ::| |: |
Db       1 MNRCWA---LFLSLCCYLRLV---SAEGDPIPEELYKML--SDHSIR---SFDDLQRLLH 49

Qy      59 SEDWKLWRCRLRLKSFTS-----MDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113
           :    |  | | |  |     ::| |   ||   ||     :   :| |      |
Db      50 GDSVDEDRAELDLNSTRSHCGGELESLSRGRRSLGEAAGSPTVAEPAMIAE------CKT 103

Qy     114 RETCVEVASELGKSTNTFFK--PPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEIS-V 170
           |   ||:  |   ||  |   |||| | || ||||  :: |  |       |: :|  |
Db     104 RTEVFEVSRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRLVQVRKIEIV 163

Qy     171 PLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDR 214
           | :   | : :|  |||       |   : ||    :| |
Db     164 RKRPVFKKATVTLEDHLACKCETVVAARP---VTRSPGSSQEQR 204


RESULT  14
A41236
placental growth factor precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 05-Nov-1999
C;Accession: A41236
R;Maglione, D.; Guerriero, V.; Viglietto, G.; Delli-Bovi, P.; Persico, M.G.
Proc. Natl. Acad. Sci. U.S.A. 88, 9267-9271, 1991
A;Title: Isolation of a human placenta cDNA coding for a protein related to the vascular
A;Reference number: A41236; MUID:92021031
A;Accession: A41236
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <MAG>
A;Cross-references: GB:X54936; NID:g35521; PIDN:CAA38698.1; PID:g35522
C;Genetics:
A;Gene: GDB:PGF
A;Cross-references: GDB:134676; OMIM:601121
A;Map position: 14q24-14q31


  Query Match             8.2%;  Score 160.5;  DB 2;  Length 149;
  Best Local Similarity   28.3%;  Pred. No. 2.5e-05;
  Matches   39;  Conservative   26;  Mismatches  56;  Indels   17;  Gaps    4;

Qy      63 KLWRCRLRLKSFTSMD-------SRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
           :|: | |:| :  ::          : || : |:       ::| :    | | |: |   |
Db       5 RLFPCFLQLLAGLALPAVPPQQWALSAGNGSS-------EVEVVP-FQEVWGRSYCRALE 56

Qy     116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
             |:| ||         | | ||:: || ||| :|:| |:   |: :: || :|
Db      57 RLVDVVSEYPSEVEHMFSPSCVSLLRCTGCCGDENLHCVPVETANVTMQLLKIR--SGDR 114

Qy     176 PELVPVKVANHTGCKCLP 193
           |  | :  : |  |:| |
Db     115 PSYVELTFSQHVRCECRP 132


RESULT  15
A56125
placental growth factor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C;Accession: A56125
R;DiSalvo, J.; Bayne, M.L.; Conn, G.; Kwok, P.W.; Trivedi, P.G.; Soderman, D.D.; Pali
J. Biol. Chem. 270, 7717-7723, 1995
A;Title: Purification and characterization of a naturally occurring vascular endothel
A;Reference number: A56125; MUID:95221439
A;Accession: A56125
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-158 <DIS>
A;Cross-references: GB:L40030; NID:g1263413; PIDN:AAA97426.1; PID:g1263414
C;Keywords: glycoprotein


  Query Match             8.0%;  Score 158;  DB 2;  Length 158;
  Best Local Similarity   29.9%;  Pred. No. 4.1e-05;
  Matches   40;  Conservative   25;  Mismatches  57;  Indels   12;  Gaps    4;

Qy      63 KLWRCRLRLKSFTSMDSR---SASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVE 119
           ||: | |:: :  :: |:   || : ||        ::| :   :| | |: | | |  |
Db       5 KLFTCFLQVLAGLAVHSQGALSAGNNST-------EMEVVP-FNEVWGRSYCRPMEKLVY 56

Qy     120 VASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELV 179
           :| |       :  | | || : || ||| :| | |:    |: |: |: :|  |       |
Db      57 IADEHPNEVSHIFSPSCVLLSRCSGCCGDEGLHCVALKTANITMQILKIP-PNRDPHSYV 115

Qy     180 PVKVANHTGCKCLP 193
           :  :    |:| |
Db     116 EMTFSQDVLCECRP 129


Search completed: May 16, 2000, 16:39:03
Job time: 7426 sec
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